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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 13:28:23 ; Search time 1435.75 seconds
(without alignments)
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Title: US-09-852-261-1

Perfect score: 517

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Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 2054640 segs, 14551402878 residues

Total number of hits satisfying chosen parameters: 4109280

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : GenEmbl:
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41: em_htgc_other:*

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517	100.0	517	6	AX147742 Sequence
2	517	100.0	517	6	AX300779 Sequence
3	467.4	90.4	523	6	AX147746 Sequence
4	467.4	90.4	523	6	AX300783 Sequence
5	377.2	73.0	471	6	AX147754 Sequence
6	377.2	73.0	471	6	AX300791 Sequence
7	355.4	68.7	444	6	HSU40870 Human alter
8	344.2	66.6	616	6	HSIGF1A
9	344.2	66.6	7260	6	AX375028 Sequence
10	344.2	66.6	7260	6	AX411095 Sequence
11	342.6	66.3	7260	6	HSIGFAC1
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13	342.6	66.3	725	9	HSIGF1
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22	325.2	62.9	539	6	AX300781 Sequence
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ALIGNMENTS

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LOCUS AX147742 517 bp DNA linear PAT 08-JUN-2001
DEFINITION Sequence 1 from Patent WO0136483.
ACCESSION AX147742
VERSION AX147742.1 GI:14346787
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.

REFERENCE
AUTHORS Goldspink, G.R. and Johnson, I.R.
TITLE Use of the insulin-like-growth factor I isoform mgf for the
treatment of neurological disorders

Pred. No. is the number of results predicted by chance to have a

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University College London (GB)
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Best Local Similarity 100.0%; Pred. No. 5e-155;
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DB 481 GATGGCATTTCGCCCAATGAATATACACAAGTAACAT 517
RESULT 2
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LOCUS AX300779
DEFINITION Sequence 1 from Patent WO0185781.
ACCESSION AX300779
VERSION AX300779.1 GI:17382060
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Goldspink,G.D. and Terenghi,G.B.
TITLE Repair of nerve damage
JOURNAL Patent: WO 0185781-A 1 15-NOV-2001;

University College London (GB) ; East Grinstead Medical Research
Trust (GB)
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BASE COUNT 150 a 130 c 139 g 98 t
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Query Match 100.0%; Score 517; DB 6; Length 517;
Best Local Similarity 100.0%; Pred. No. 5e-155;
Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 481 GATGGCATTTCGCCCAATGAATATACACAAGTAACAT 517
RESULT 3
AX147746 523 bp DNA linear PAT 08-JUN-2001
LOCUS AX147746
DEFINITION Sequence 5 from Patent WO0136483.
ACCESSION AX147746
VERSION AX147746.1 GI:14346791
KEYWORDS
SOURCE rabbit.
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE 1 (bases 1 to 523)
AUTHORS Goldspink,G.R. and Johnson,I.R.
TITLE Use of the insulin-like-growth factor I isoform mgf for the
treatment of neurological disorders

JOURNAL Patent: WO 0136483-A 5 25-MAY-2001;
University College London (GB)
FEATURES Location/Qualifiers
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BASE COUNT 154 a 129 c 142 g 98 t
ORIGIN

Query Match 90.4%; Score 467.4; DB 6; Length 523;
Best Local Similarity 96.2%; Pred. No. 4.8e-139;
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

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RESULT 4
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LOCUS AX300783
DEFINITION Sequence 5 from Patent WO0185781.
ACCESSION AX300783
VERSION AX300783.1 GI:17382064
KEYWORDS
SOURCE
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE
AUTHORS Goldspink,G.D. and Terenghi,G.B.
TITLE Repair of nerve damage
JOURNAL Patent: WO 0185781-A 5 15-NOV-2001;

University College London (GB) ; East Grinstead Medical Research
Trust (GB)
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Query Match 90.4%; Score 467.4; DB 6; Length 523;
Best Local Similarity 96.2%; Pred. No. 4.8e-139;
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

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RESULT 5
AX147754 471 bp DNA linear PAT 08-JUN-2001
LOCUS AX147754
DEFINITION Sequence 13 from Patent WO0136483.
ACCESSION AX147754
VERSION AX147754.1 GI:14348552
KEYWORDS
SOURCE
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE
AUTHORS Goldspink,G.R. and Johnson,I.R.
TITLE Use of the insulin-like-growth factor I isoform mlf for the
treatment of neurological disorders

JOURNAL Patent: WO 0136483-A 13 25-MAY-2001;
University College London (GB)
FEATURES Location/Qualifiers
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DB 432 AGATGGCATTTCCCAATGAATACACAAGTAACAT 469
RESULT 6
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LOCUS Sequence 13 from Patent WO0185781.
DEFINITION AX300791
ACCESSION AX300791
VERSION GI:17382072
KEYWORDS
SOURCE Rabbitt.
ORGANISM Oryctolagus cuniculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
REFERENCE
AUTHORS Goldspink, G.D. and Terenghi, G.B.
TITLE Repair of nerve damage
JOURNAL Patent: WO 0185781-A 13 15-NOV-2001;

University College London (GB) ; East Grinstead Medical Research
Trust (GB)
FEATURES Location/Qualifiers
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BASE COUNT 132 a 118 c 131 g 90 t
ORIGIN
Query Match 73.0%; Score 377.2; DB 6; Length 471;
Best Local Similarity 87.8%; Pred. No. 5.3e-110;
Matches 455; Conservative 0; Mismatches 13; Indels 50; Gaps 2;
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DB 432 AGATGGCATTTCCCAATGAATACACAAGTAACAT 469
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HS040870 444 bp mRNA linear PRI 05-APR-1996
LOCUS Human alternatively spliced human insulin-like growth factor-I
DEFINITION (IGF-I) mRNA, partial cds.
ACCESSION U40870
VERSION U40870.1 GI:1100902
KEYWORDS
SOURCE Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
AUTHORS Chew, S.L., Lavender, P., Clark, A.J. and Ross, R.J.
TITLE An alternatively spliced human insulin-like growth factor-I

transcript with hepatic tissue expression that diverts away from the mitogenic IREL peptide
 JOURNAL Endocrinology 136 (5), 1939-1944 (1995)
 MEDLINE 95237119
 PUBMED 7720641
 REFERENCE 2 (bases 1 to 444)
 AUTHORS Chew, S.L.
 TITLE Direct Submission
 JOURNAL Submitted (20-NOV-1995) Sherr L. Chew, Endocrinology, St Bartholomew's Hospital Medical College, West Smithfield, London, EC1A 7BE, UK

FEATURES
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 /db_xref="GI:1100903"
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BASE COUNT 107 a 125 c 125 g 87 t
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Query Match 68.7%; Score 355.4; DB 9; Length 444;
 Best Local Similarity 99.7%; Pred. No. 5,6e-103; Indels 0; Gaps 0;
 Matches 356; Conservative 0; Mismatches 1;

QY 1 GGACCGGAGACGCTGCGGGGCTGAGCTGTGATGCTCTTCAGTTCGTGTTGGAGAC 60
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 DB 88 GGACCGGAGACGCTGCGGGGCTGAGCTGTGATGCTCTTCAGTTCGTGTTGGAGAC 147
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 QY 61 AGGGGCTTTATTATTCACACAGCCCAAGGGATATGCTCCAGCATGTCGAGGGCGCTAG 120
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 DB 328 ATGCCCAAGACCAAGATATCAGCCCCCATCTACCAACAAGACGAGTCTAGAGA 387
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QY 301 AGGAAGAGAGTTCATTGACAGACACAGTAGAGGAGTGCAGAACAGACTA 357
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 DB 388 AGGAAGAGAGTTCATTGACAGACACAGTAGAGGAGTGCAGAACAGACTA 444
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RESULT 8
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 H.sapiens mRNA for IGF-1a.
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 X56773.1 GI:32989
 IGF-1 gene.
 Homo sapiens
 SOURCE
 ORGANISM
 Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
 AUTHORS Sandberg-Nordqvist, A.C., Stahlbom, P.A., Lake, M. and Sara, V.R.
 TITLE Characterization of two cDNAs encoding insulin-like growth factor 1
 (IGF-1) in the human fetal brain
 JOURNAL Brain Res. Mol. Brain Res. 12 (1-3), 275-277 (1992)
 MEDLINE 92186627
 PUBMED 1372070

REFERENCE
 AUTHORS Sandberg-Nordqvist, A.C.
 TITLE Direct Submission
 JOURNAL Submitted (19-NOV-1990) A.C. Sandberg Nordqvist, KAROLINSKA INST'S
 DEPT OF PATHOLOGY, KAROLINSKA HOSPITAL, BOX 605 00, S-104 01
 STOCKHOLM, SWEDEN

REFERENCE
 AUTHORS Sandberg-Nordqvist, A.C., Stahlbom, P.A., Reinecke, M., Collins, V.P.,
 von Holst, H. and Sara, V.
 TITLE Characterization of Insulin-like growth factor 1 in human primary
 brain tumors
 JOURNAL Cancer Res. 53 (11), 2475-2478 (1993)
 MEDLINE 93265440
 PUBMED 8495408

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 Matches 455; Conservative 0; Mismatches 13;

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QY 121 ACAGGCTATGCTGATGATGCTGCTCCGAGCTGATCTAAGGAGGCTGAGATGAT 180
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QY 361 GATGTA-GAAGACCCCTCTGAGAGTGAAGAGGACAGGCGCAGGACCCCTTGTCTC 419
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Db 456 GATGTAAGAGACCCCTCTGAGAGTGAAGAGTGAAGTGCAGGACCCAGATCTTGTCTC 515
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QY 420 TGCAC-AGTTACCTG-TAAACATTGGAATACGCGCCAAAAAATAGTTGATCATTTC 477
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Db 516 TGCACAGTGTACCTGTTAAACTTTGAAACACCTACCAAAAAATAGTTGATCATTTC 575
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Db 576 AAGATGGGCTTCCCCCAATGAATACACAGTAACAT 616
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RESULT 9
AX375028 7260 bp DNA linear PAT 01-MAR-2002
LOCUS Sequence 31 from Patent WO0210436.
ACCESSION AX375028
VERSION AX375028.1 GI:19196860
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1 Baak,J. and Mutter,G.L.
TITLE Prognostic classification of breast cancer
JOURNAL Patent: WO 0210436-A 31 07-FEB-2002;
THE BRIGMAN AND WOMEN'S HOSPITAL, INC. (US) : Baak, Jan (US)
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Best Local Similarity 87.3%; Pred. No. 3.4e-99;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;
QY 1 GGAACGGAGAGGCTTGGGGGCTGAGCTGATGATGCTTTCACTTCTGCTGTGAGAG 60
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Db 311 GGAACGGAGAGGCTTGGGGGCTGAGCTGATGATGCTTTCACTTCTGCTGTGAGAG 370
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QY 61 AGGGGCTTTTATTTAACAAGCCCAAGGCTATGCTCCAGACAGTGGAGGCGCTCAG 120
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RESULT 10
AX411095 7260 bp DNA linear PAT 14-JUN-2002
LOCUS Sequence 3742 from Patent WO0229103.
ACCESSION AX411095
VERSION AX411095.1 GI:21443800
KEYWORDS
SOURCE human.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
1 Alvarez,C., Horne,D., Pares-da-Silva,S. and Vockley,J.G.
TITLE Gene expression profiles in liver cancer
JOURNAL Patent: WO 0229103-A 3742 11-APR-2002;
GENE LOGIC INC (US)
FEATURES
Location/Qualifiers
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/note="EMBL/GenBank Accession No. X57025"
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Query Match 66.6%; Score 344.2; DB 6; Length 7260;
Best Local Similarity 87.3%; Pred. No. 3.4e-99;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;
QY 1 GGAACGGAGAGGCTTGGGGGCTGAGCTGATGATGCTTTCACTTCTGCTGTGAGAG 60
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Db 311 GGAACGGAGAGGCTTGGGGGCTGAGCTGATGATGCTTTCACTTCTGCTGTGAGAG 370
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Db 622 GATGTAGGAAGACCTCTTGAGAGTGAAGAGACAGACCCGACGAGATCCTTTGCTC 681
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Db 682 TGCACAGTACTCTGTTAACTTTGGAACCTTACCAAAAATAAGTTGATCACTTTA 741
QY 478 AAGAT-GGCATTTCCTCCCAATGAATACACAGTAACAT 517
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Db 742 AAGATGGCGTTTCCCCCAATGAATACACAGTAACAT 782

RESULT 11
HSIGFACI 7260 bp mRNA linear PRI 17-FEB-1992
LOCUS Human IGF-I mRNA for insulin-like growth factor I.
DEFINITION X57025
ACCESSION X57025.1 GI:33007
KEYWORDS Insulin-like growth factor I.
SOURCE Homo sapiens.
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 7260)
AUTHORS Steenbergh, P. H.
TITLE Direct Submission
JOURNAL Submitted (18-DEC-1990) P. H. Steenbergh, LAB FOR PHYSIOLOGICAL
MEDLINE CHEMISTRY, UNIVERSITY OF UTRECHT, VONDELAN 24 A, 3521 GG UTRECHT,
THE NETHERLANDS
FEATURES 2 (bases 1 to 7260)
REFERENCE Steenbergh, P. H., Koonen-Reemst, A. M., Cleutjens, C. B. and
AUTHORS Susenbach, J. S.
TITLE Complete nucleotide sequence of the high molecular weight human
JOURNAL IGF-I mRNA
MEDLINE Blochys. Res. Commun. 175 (2), 507-514 (1991)
PUBMED 91207342
FEATURES 2018498
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BASE COUNT 2330 a 1415 c 1240 g 2275 t
ORIGIN

Query Match 66.6%; Score 344.2; DB 9; Length 7260;
Best Local Similarity 87.3%; Pred. No. 3.4e-99;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

QY 1 GGACCGGACACGCTCTGCGGGGCTGAGCTGTGATGCTCTTCATGCTGTGTGAGAC 60
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Db 311 GGACCGGACACGCTCTGCGGGGCTGAGCTGTGATGCTCTTCATGCTGTGTGAGAC 370
QY 61 AGGGGCTTTATTTCACAGCCACAGGGTATGGCTCCAGAGTCGAGGCGGCTCAG 120
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Db 371 AGGGGCTTTATTTCACAGCCACAGGGTATGGCTCCAGAGTCGAGGCGGCTCAG 430
QY 121 ACAGGATCGTGAGTGTGCTGCTTCGAGAGCTGTATTAAGAGGCTGCAGATGTAT 180
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Db 431 ACAGGATCGTGAGTGTGCTGCTTCGAGAGCTGTATTAAGAGGCTGCAGATGTAT 490
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Db 491 TGGCACCCTCTCAAGCTGCCAAGTCACTGCTGTCCGTCGACGCGCACACCGAC 550
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Db 551 ATGCCCAAGACCCAG----- 565
QY 301 AGGAAGAGTACATTGAGACACAAAGTAGAGGAGTGCAGAAACAGACTACG 360
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Db 566 ----AAGGAAGTACATTGAGACACAAAGTAGAGGAGTGCAGAAACAGACTACG 621
QY 361 GATGTA-GAAGACCTCTTGAGAGTGAAGAGACAGACCCGACGAGACCTTTGCTC 419
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Db 622 GATGTAGGAAGACCTCTTGAGAGTGAAGAGACAGACCCGACGAGATCCTTTGCTC 681
QY 420 TGCAC-AGTACTCTG-TAAACATTGGAATCCGCCCAAAAATAAGTTGATCACTTC 477
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Db 742 AAGATGGCGTTTCCCCCAATGAATACACAGTAACAT 782

[illegible]

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Db	467	GATGTAAG	AAACCCCTCTCTG	AGAGTAGAAG	AGTACATGCAC	CCGCAAGATCTT	CTCTC	526	
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	RESULT 15		
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LOCUS	HUMIGFI	1076 bp	mRNA linear cds.
DEFINITION	Human insulin-like growth factor mRNA, complete cds.		
ACCESSION	M27544		
VERSION	M27544.1 GI:184829		
KEYWORDS	insulin-like growth factor.		
SOURCE	Human liver, cDNA to mRNA, clones lambda-TG[03_04_05].		
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 1076) Le Bouc,Y., Dreier,D., Jaeger,F., Binoux,M. and Sondenmeier,P. Complete characterization of the human IGF-I nucleotide sequence isolated from a newly constructed adult liver CDNA library FEBS Lett. 196 (1), 108-112 (1986)		
TITLE			
JOURNAL			
MEDLINE			
PUBMED	86108910		
FEATURES	2935423		
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ORIGIN	Chromosome 7p13-p12.		
Query Match	66.3%; Score 342.6;		
	DB 9; Length 1076;		

Best Local Similarity 87.1%; Pred. No. 8.5e-99;
Matches 454; Conservative 0; Mismatches 14; Indels 53; Gaps 5;

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Oy	181	TGCGCACCCCTCAAGCTGCCAAGTACGTGCTGTGTGCTGGCCACAGCGCACACCGAC	240
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Oy	301	AGGAAAGGAGTACATTTTGAAGACACAGATAGAGGAGTGCAGAGAAACAGAACTACAG	360
Oy	361	GATGTA-GAAGACCCCTTCTGAGGAGTGAAGAAAGACAGCCGACCGAGACCTTTGCTC	419
Oy	420	TGCAC-AGTTTACCTG-TAAACATTGAAATACCGGCCCAAAAAATTAAGTTTGTATCATTTTC	477
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Oy	1803	ATGAGTGGGGGTTTCCCGCAATGAATACAGTAACAT	1862
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 09:07:57 ; Search time 156.935 Seconds
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Gapop 10.0, Gapext 1.0

Searched: 2185239 seqs, 112599159 residues

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Minimum DB seq length: 0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517	100.0	517	22	AAD06398 Human IGF-I isoform
2	517	100.0	517	24	AA016877 Human mechano-growth
3	467.4	90.4	523	22	AA06400 Rabbit IGF-I isoform
4	467.4	90.4	523	24	AA016877 Rabbit mechano-gro
5	467.4	90.4	553	18	AA04893 Rabbit insulin-like
6	377.2	73.0	471	22	AA06405 Rabbit liver-type
7	377.2	73.0	471	24	AA016884 Rabbit insulin-like
8	344.2	66.6	818	8	AA070436 Sequence encoding
9	344.2	66.6	7260	24	ABR64583 Human CDNA differe

10	344.2	66.6	7260	24	ABN97244 Gene #3742 used to
11	344.2	66.6	7260	24	ABR64812 Human benign prostr
12	344.2	66.6	7260	24	ABR33504 Human endometrial
13	344.2	66.6	7260	24	ABR33561 Gene IGF-I differer
14	342.6	66.3	777	18	AA084894 Human insulin-like
15	339.4	65.6	622	7	AA060490 Human prepro-somat
16	325.2	62.9	539	22	AAD06399 Rat IGF-I isoform
17	325.2	62.9	539	22	AA016878 Rat mechano-growth
18	308.6	56.7	1136	8	AA070435 Sequence encoding
19	286.4	55.4	3599	19	AAV50428 Plasmid pIG0352 10
20	286.4	55.4	3599	19	AAV504796 Actual sequence of
21	286.4	55.4	3600	19	AAV50427 Plasmid pIG0552 up
22	286.4	55.4	3600	19	AAV504795 Expected sequence
23	286.4	55.4	5707	20	AA088055 Plasmid pIG0335 DN
24	286.4	55.4	6345	20	AA088054 Plasmid pIG0100A D
25	285.4	55.2	612	22	AA016895 Human cDNA encodin
26	271.2	52.5	978	14	AA041804 Sequence encoding
27	258.4	50.0	317	24	AA016882 Human insulin-like
28	258.4	50.0	318	22	AAD06403 Human liver-type I
29	258.4	50.0	462	19	AAV50426 Human IGF-I encodi
30	258.4	50.0	462	19	AAV40794 Human IGF-I coding
31	258.4	50.0	462	24	AB016898 Human polynucleoti
32	252.6	48.9	1052	20	AA027498 Rat liver form of
33	247.8	47.9	487	22	AAD06404 Rat liver-type IGF
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35	210	40.6	210	24	ABR03146 Native mature IGF-
36	208.4	40.3	237	12	AA013568 Beta-gal/IGF-1 fus
37	208.4	40.3	238	12	AA013569 Recombinant botull
38	208.4	40.3	2862	19	AAV56283 Bovine alpha lacta
39	204.6	39.6	4532	24	AA032015 Human insulin-like
40	203.6	39.4	210	24	AA032016 Synthetic human IG
41	202.8	39.2	240	13	AA023303 Killer toxin leade
42	202.8	39.2	230	18	AA063526 Seq ID 1 used in t
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ALIGNMENTS

RESULT 1
ID AAD06398
AAD06398 standard, CDNA; 517 BP.

XX AAD06398;

DT 10-AUG-2001 (first entry)

XX Human IGF-I isoform mechano-growth factor (MGF) cDNA.

XX Human, IGF-I isoform; Insulin-like Growth Factor-I; MGF;
KW mechano-growth factor; neurological disorder; neurodegenerative disorder;
KW amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
KW poliomyelitis; post-polio syndrome; toxin; motoneuron disorder;
KW nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
KW sex-linked muscular dystrophy; peripheral neuropathy;
KW Alzheimer's disease; Parkinson's disease; ss.

XX Homo sapiens.

XX Key Location/Qualifiers
XX CDS 1..333
XX /tag= a
XX /product= "Mechano-growth factor (MGF)"
XX /note= "This region comprises exons 3-6. The CDS does
XX not include start codon"
XX /partial

PN WO200136483-A1.

XX 25-MAY-2001.

PF 15-NOV-2000; 2000MO-GB04354.
 XX 15-NOV-1999; 99GB-0026968.
 XX (UNLO) UNIV COLLEGE LONDON.
 PA Goldslink G, Johnson I;
 PI WPI: 2001-355620/37.
 DR P-PSDB: AAE02447.
 XX
 PT Use of mechano-growth factor, an isoform of insulin-like growth
 PT Factor-I, capable of reducing motoneuron loss, in the manufacture of a
 PT medicament for the treatment of neurological disorder -
 XX
 PS Claim 4: Page 49-50: 66pp; English.

CC The present invention relates to use of mechano-growth factor (MGF),
 CC an insulin-like growth factor-I (IGF-I) isoform in the manufacture of a
 CC medicament for the treatment of neurological disorder. The MGF is capable
 CC of reducing motoneuron loss by 20% or greater in response to nerve
 CC avulsion, and effects motoneuron rescue, preferably adult motoneuron
 CC rescue. The MGF polynucleotide and polypeptide are useful in the
 CC manufacture of a medicament for the treatment of a neurological disorder,
 CC including a disorder of motoneurons and/or neurodegenerative disorder,
 CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
 CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
 CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
 CC toxin, motoneuron trauma, a motoneuron lesion or nerve damage, an
 CC injury that affects motoneurons, motoneuron loss associated with aging,
 CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
 CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
 CC The present sequence is human IGF-I isoform MGF cDNA. MGF is a muscle
 CC isoform having extracellular (Ec) domain, hence also referred as
 CC IGF-I-Ec. The MGF protein comprises amino acid sequences encoded by
 CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
 CC of MGF.
 CC
 XX SQ Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;

Query Match 100.0%; Score 517; DB 22; Length 517;
 Best Local Similarity 100.0%; Pred. No. 2e-146;
 Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGACCGGAGAGAGCTGCGGGGCTGAGCTGATGCTCTTCAGTTGCTGTGGAGAC 60
 DB 1 GGACCGGAGAGAGCTGCGGGGCTGAGCTGATGCTCTTCAGTTGCTGTGGAGAC 60
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 DB 181 TCGGACACCCCTTAACCTGCGCAAGTCACTGCTGTGCTGCGCCAGCGCAACCGAC 240
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 DB 241 ATGCCCAAGACCCAGAGATATGAGCCCATCTACCAACAAGAACAGCAAGCTCTCAGAGA 300
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 DB 301 AGGAAGAGAGTACTTTGAGAGACACAAAGTAGAGGGAGTCAAGAAACAGAACTACAG 360
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 DB 361 GATGTAGAGAGACCCCTTCTGAGAGAGTGAAGAGAGCCACCGCAGAGACCCCTTGTCTCT 420
 QY 421 GCACAGTTACCTGTAAACATTGGATACCGGCGCAAAAATAAGTTGATCACTTTCAAA 480

DB 421 GCACAGTTACCTGTAAACATTGGATACCGGCGCAAAAATAAGTTGATCACTTTCAAA 480
 QY 481 GATGGCATTTCCCAATGAAATACAAAGTAACAT 517
 DB 481 GATGGCATTTCCCAATGAAATACAAAGTAACAT 517

RESULT 2
 AAS16877 standard; cDNA; 517 BP.
 ID AAS16877;
 AC AAS16877;
 XX 25-FEB-2002 (first entry)
 DE Human mechano-growth factor (MGF) cDNA.
 KW Human; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
 KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;
 KW muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;
 KW nerve avulsion.
 XX Homo sapiens.
 OS
 XX
 FH Key Location/Qualifiers
 FT CDS 1..333
 FT /*tag= a
 FT /product= "Human MGF"
 FT /partial
 FT /note= "No start codon"
 FT exon 1..76
 FT /*tag= b
 FT /number= 3
 FT exon 77..259
 FT /*tag= c
 FT /number= 4
 FT exon 260..307
 FT /*tag= d
 FT /number= 5
 FT exon 308..330
 FT /*tag= e
 FT /number= 6

XX WO200185781-A2.
 XX 15-NOV-2001.
 PD 10-MAY-2001; 2001MO-GB02054.
 XX 10-MAY-2000; 2000GB-0011278.
 PR 10-MAY-2000; 2000GB-0011278.
 XX
 PA (UNLO) UNIV COLLEGE LONDON.
 PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.
 XX Goldslink G, Terengh G;
 PI WPI: 2002-055585/07.
 DR P-PSDB: AA010539.
 XX

PT Use of insulin-like growth factor I (IGF-I) isoform known as
 PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
 PT ability to reduce motoneuron loss in response to nerve avulsion, to
 PT treat nerve damage -
 XX
 PS Claim 11: Fig 5: 65pp; English.

CC The invention relates to the use of an insulin-like growth factor I
 CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
 CC of a medicament for treating nerve damage in the peripheral nervous
 CC system, or for treating nerve damage by localising MGF at the site of
 CC damage. The nerve damage may include severing of a nerve. The treatment
 CC may be combined with another treatment (such as a polypeptide growth

CC factor other than MGF) that prevents or diminishes degeneration of the
 CC target organ (for example, muscle) which the damaged nerve innervates,
 CC whereby the treatment of the muscle with MGF or a polynucleotide encoding
 CC MGF prevents or diminishes degeneration. The method is useful for
 CC treating neurological disorders, preferably motoneuron disorders. These
 CC methods can reduce motoneuron loss by 20% or greater in response to nerve
 CC avulsion. This sequence represents cDNA encoding the human MGF.

CC Sequence 517 BP; 150 A; 130 C; 139 G; 98 T; 0 other;

Query Match 100.0%; Score 517; DB 24; Length 517;
 Best Local Similarity 100.0%; Pred. No. 2e-146;
 Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 GGAGCCGAGAGAGCTCTCGGAGCTGAGCTGATGATCTTATGATGATGAGAGAC 60
 DB 1 GGAGCCGAGAGAGCTCTCGGAGCTGAGCTGATGATCTTATGATGATGAGAGAC 60
 QY 61 AGGGGCTTTTATTTCACAAAGCCACAGGGTATGGCTCCAGAGTCGGAGGCGCTCAG 120
 DB 61 AGGGGCTTTTATTTCACAAAGCCACAGGGTATGGCTCCAGAGTCGGAGGCGCTCAG 120
 QY 121 ACAGGATGCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 DB 121 ACAGGATGCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
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 QY 241 ATGCCCAAGAGCCAGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 300
 DB 241 ATGCCCAAGAGCCAGAGTATGAGTATGAGTATGAGTATGAGTATGAGTATGAG 300
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 DB 301 AGGAAAGAGTATGATGATGATGATGATGATGATGATGATGATGATGATGATG 360
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 DB 361 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 420
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 DB 481 GATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 517

RESULT 3
 AAD06400
 ID AAD06400 standard; cDNA; 523 BP.

AC AAD06400;

DE 10-AUG-2001 (first entry)

XX Rabbit IGF-I isoform mechano-growth factor (MGF) cDNA.

XX Rabbit; IGF-I isoform; insulin-like growth factor-I; MGF;

XX mechano-growth factor; neurological disorder; neurodegenerative disorder;

XX amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;

XX poliomyelitis; post-polio syndrome; toxin; motoneuron disorder;

XX nerve damage; autosomal muscular dystrophy; diabetic neuropathy;

XX Alzheimer's disease; Parkinson's disease; ss.

XX Oryctolagus cuniculus.

XX Key Location/Qualifiers

FT CDS 1..336

FT /*tag= a "mechano-growth factor (MGF)"
 FT /product= "mechano-growth factor (MGF)"
 FT /note= "This region comprises exons 3-6. The CDS does
 FT not include start codon"
 FT /partial

PN W0200136483-A1.

PD 25-MAY-2001.

PF 15-NOV-2000; 2000WO-GB04354.

PR 15-NOV-1999; 99GB-0026968.

PA (UNLO) UNIV COLLEGE LONDON.

PI Goldslink G, Johnson I;

DR MPI; 2001-355620/37.

XX P-PSDB; AAE02449.

PT Use of mechano-growth factor, an isoform of insulin-like growth

PT Factor-I, capable of reducing motoneuron loss, in the manufacture of a

PS Claim 4; Page 53-54; 66pp; English.

CC The present invention relates to use of mechano-growth factor (MGF),
 CC an insulin-like growth factor-I (IGF-I) isoform in the manufacture of a
 CC medicament for the treatment of neurological disorder. The MGF is capable
 CC of reducing motoneuron loss by 20% or greater in response to nerve
 CC avulsion, and effects motoneuron rescue, preferably adult motoneuron
 CC rescue. The MGF polynucleotide and polypeptide are useful in the
 CC manufacture of a medicament for the treatment of a neurological disorder,
 CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
 CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
 CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
 CC toxin, motoneuron trauma, a motoneuron lesion or nerve damage, an
 CC injury that affects motoneurons, motoneuron loss associated with aging,
 CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
 CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
 CC The present sequence is rabbit IGF-I isoform MGF cDNA. MGF is a muscle
 CC isoform having extracellular (EC) domain, hence also referred as
 CC IGF-I-EC. The MGF protein comprises amino acid sequences encoded by
 CC nucleic acid sequence of IGF-I exons 4, 5 and 6 in the reading frame
 CC of MGF.

SO Sequence 523 BP; 154 A; 129 C; 142 G; 98 T; 0 other;

Query Match 90.4%; Score 467.4; DB 22; Length 523;
 Best Local Similarity 96.2%; Pred. No. 2.1e-131;
 Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

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 DB 1 GGAGCCGAGAGAGCTCTCGGAGCTGAGCTGATGATGATGATGATGATGATGATG 60
 QY 61 AGGGGCTTTTATTTCACAAAGCCACAGGGTATGGCTCCAGAGTCGGAGGCGCTCAG 120
 DB 61 AGGGGCTTTTATTTCACAAAGCCACAGGGTATGGCTCCAGAGTCGGAGGCGCTCAG 120
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 DB 121 ACAGGATGCTGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
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 OY 477 CAAGATGGCATTTCCCAATGAATACACAGTAACAT 517
 DB 481 CAAGATGGCATTTCCCAATGAATACACAGTAACAT 521

RESULT 4
 AAS16879
 ID AAS16879 standard; cDNA; 523 BP.
 AC AAS16879;

XX 25-FEB-2002 (first entry)
 DE Rabbit mechano-growth factor (MGF) cDNA.

KW Rabbitt; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
 KW neuroprotective; nerve damage; peripheral nervous system; nerve severing;
 KW muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;
 KW nerve avulsion.
 XX Oryctolagus cuniculus.

FH Key Location/Qualifiers
 FT CDS 1..336
 FT /*tag= a
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W0200185781-A2.

XX 15-NOV-2001.

XX 10-MAY-2001: 2001MO-GB02054.

XX 10-MAY-2000: 2000GB-0011278.

PA (UNLO) UNIV COLLEGE LONDON.
 PA (EGRI-) EAST GRINSTEAD MEDICAL RES TRUST.

PI Goldspink G, Terenghi G;

XX WPI: 2002-055585/07.

DR P-PSDB; AAU10561.

XX Use of insulin-like growth factor I (IGF-I) isoform known as
 PT mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has
 PT ability to reduce motoneuron loss in response to nerve avulsion, to

FT treat nerve damage
 XX Disclosure: Fig 7; 65pp; English.
 XX The invention relates to the use of an insulin-like growth factor I
 CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
 CC of a medicament for treating nerve damage in the peripheral nervous
 CC system, or for treating nerve damage by localising MGF at the site of
 CC damage. The nerve damage may include severing of a nerve. The treatment
 CC may be combined with another treatment (such as a polypeptide growth
 CC factor other than MGF) that prevents or diminishes degeneration of the
 CC target organ (for example, muscle) which the damaged nerve innervates,
 CC whereby the treatment of the muscle with MGF or a polypeptide encoding
 CC MGF prevents or diminishes degeneration. The method is useful for
 CC treating neurological disorders, preferably motoneuron disorders. These
 CC methods can reduce motoneuron loss by 20% or greater in response to nerve
 CC avulsion. This sequence represents cDNA encoding the rabbit MGF.

SQ Sequence 523 BP; 154 A; 129 G; 142 C; 98 T; 0 other;

Query Match 90.4%; Score 467.4; DB 24; Length 523;
 Best Local Similarity 96.2%; Preg. No. 2.1e-131;
 Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

OY 1 GGACCGAGAGCGCTCTGCGGGGCTGAGCTGATGATGCTCTTCACTTGTGTGAGAC 60
 DB 1 GGACCGAGAGCGCTCTGCGGGGCTGAGCTGATGATGCTCTTCACTTGTGTGAGAC 60
 OY 61 AGGGGCTTTTATTCACAAACCCACAGGATGATGCTCCAGATCGGAGGCGCCCTCAG 120
 DB 61 AGGGGCTTTTATTCACAAACCCACAGGATGATGCTCCAGATCGGAGGCGCCCTCAG 120
 OY 121 ACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 DB 121 ACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 OY 181 TGGCGACCCCTTCAAGAGCTGCCAAGTCACTGCTCTGCTGCTGCCACGCCACACCGAC 240
 DB 181 TGGCGACCCCTTCAAGAGCTGCCAAGTCACTGCTCTGCTGCTGCCACGCCACACCGAC 240
 OY 181 TGTGACCCCTTCAAGAGCTGCCAAGTCACTGCTCTGCTGCTGCCACGCCACACCGAC 240
 DB 181 TGTGACCCCTTCAAGAGCTGCCAAGTCACTGCTCTGCTGCTGCCACGCCACACCGAC 240
 OY 241 ATGCCCAAGACCCCAAGATATCAGCCCGCATCTCCCAAGACAGACAGATGCTCA---G 297
 DB 241 ATGCCCAAGACCCCAAGATATCAGCCCGCATCTCCCAAGACAGACAGATGCTCA---G 297
 OY 241 ATGCCCAAGACCCCAAGATATCAGCCCGCATCTCCCAAGACAGACAGATGCTCA---G 297
 DB 241 ATGCCCAAGACCCCAAGATATCAGCCCGCATCTCCCAAGACAGACAGATGCTCA---G 297
 OY 298 AGAAGAAAGGAGTACATTGTAAGACACACAGTAGAGGAGTGCAGAGAAACAAGACTA 357
 DB 301 AGAAGAAAGGAGTACATTGTAAGACACACAGTAGAGGAGTGCAGAGAAACAAGACTA 360
 OY 358 CAGGATGTA-GAAGACCCCTTCTGAGAGTGAAGAGAGGACGACCGAGACCTTTG 416
 DB 361 CAGGATGTAAGAGACCCCTTCTGAGAGTGAAGAGAGGACGACCGAGACCTTTG 420
 OY 417 CTCTGCACAGTTACTGTAACATTGGAATACCGGCCCAAAAATAAGTTGATCACTTT 476
 DB 421 CTCTGCACAGTTACTGTAACATTGGAATACCGGCCCAAAAATAAGTTGATCACTTT 480
 OY 477 CAAGATGGCATTTCCCAATGAATACACAGTAACAT 517
 DB 481 CAAGATGGCATTTCCCAATGAATACACAGTAACAT 521

RESULT 5
 AAT84893
 ID AAT84893 standard; cDNA; 553 BP.

XX AAT84893;

XX 14-APR-1998 (first entry)

DE Rabbit insulin like growth factor 1 encoding cDNA.

KW Insulin like growth factor 1; IGF-1; Ec peptide; muscle disorder;
 KW heart; neuromuscular disease; primer; ss.

XX Oryctolagus cuniculus.
 XX Key Location/Qualifiers
 FT CDS 1..366
 FT /*tag= a
 FT /product= "IGF-1"
 XX WO9733997-A1.
 XX 18-SEP-1997.
 XX 11-MAR-1997; 97WO-GB00658.
 XX 11-MAR-1996; 96GB-0005124.
 XX (UNLO) ROYAL FREE HOSPITAL SCHOOL MED.
 XX Goldslink G;
 XX WPI; 1997-470877/43.
 XX P-PSDB; AAM23301.
 XX
 XX Use of insulin like growth factor I characterised by presence of Ec
 XX peptide - to treat humans or animals, particularly muscle disorders,
 XX heart conditions or neuromuscular diseases
 XX
 XX Disclosure: Fig 3; 33pp; English.
 XX
 XX A use of insulin like growth factor I (IGF-1) has been developed, and
 XX is characterised by the presence of the Ec peptide, or a functional
 XX equivalent, in the treatment or therapy of a human or animal. The IGF-1
 XX polypeptide can be used to treat muscular disorders, e.g. Duchenne or
 XX Becker muscular dystrophy, autosomal dystrophies and related progressive
 XX skeletal muscle weakness and wasting, muscle atrophy in ageing humans,
 XX spinal cord injury induced muscle atrophy and neuromuscular diseases,
 XX and cardiac disorders, e.g. diseases where promotion of cardiac muscle
 XX protein synthesis is a beneficial treatment, cardiomyopathies and acute
 XX heart failure or insult, specifically myocarditis or myocardial
 XX infarction. It can also be used to promote bone fracture healing and
 XX maintenance of bone in old age. The present sequence encodes rabbit
 XX IGF-1 used in the present specification.
 XX
 XX Sequence 553 BP; 159 A; 142 C; 147 G; 105 T; 0 other;
 XX
 XX Query Match 90.4%; Score 467.4; DB 18; Length 553;
 XX Best Local Similarity 96.2%; Pred. No. 2.1e-131;
 XX Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;
 XX
 XX 1 GGACCGGAGACGCTGTGGGGGCTGAGCTGTGATGCTCTTCAGTTCGTGTGGAGAC 60
 XX |||||||
 XX 31 GGACCGGAGACGCTGTGGGGGCTGAGCTGTGATGCTCTTCAGTTCGTGTGGAGAC 90
 XX |||||||
 XX 61 AGGGGCTTTATTTAAACAAGCCACAGGATATGGCTCCAGAGCGGAGGCGGCTAG 120
 XX |||||||
 XX 91 AGGGGCTTTATTTAAACAAGCCACAGGATATGGCTCCAGAGCGGAGGCGGCTAG 150
 XX |||||||
 XX 121 ACAGGATCGATGATGATGCTGTCTCGAGAGCTGTGATCTAAGAGGCTGAGATGTAT 180
 XX |||||||
 XX 151 ACAGGATCGATGATGATGCTGTCTCGAGAGCTGTGATCTAAGAGGCTGAGATGTAT 210
 XX |||||||
 XX 181 TGGGCAAGGCTTCAAGCTTCCAGAGTATGCTGTCTCGAGAGCGGAGGCGGCTAG 240
 XX |||||||
 XX 211 TGTGCACCCCTCAAGCGGCAAGGAGCGCCCTCGCTCCGTCGCGCCAGGCGCACCGAC 270
 XX |||||||
 XX 241 ATGCCCAAGACCAAGATATCAGCCCATCTACCAACAACAACAGAGTCTCA--G 297
 XX |||||||
 XX 271 ATGCCCAAGATCAGAGATATCAGCCCATCTACCAACAACAAGATGAGTCTAGAGG 330
 XX |||||||
 XX 298 AGAAGGAAAGAGATGATTTGAAGAACCAAGTGAAGGAGTGCAGGAAACAAGACTA 357
 XX |||||||
 XX 331 AGAAGGAAAGAGATGATTTGAAGAACCAAGTGAAGGAGTGCAGGAAACAAGACTA 390
 XX |||||||

XX 358 CAGATGTA-GAAGACCCCTTCTGAGAGTGAAGAGACAGGCCACCCAGACCCCTTTG 416
 XX |||||||
 XX 391 CAGATGTAAGAGACCCCTTCTGAGAGTGAAGAGAGAGAGGCCACCCAGACCCCTTTG 450
 XX |||||||
 XX 417 CTCTGACAGTACCTGTAACATGGAATACCGGCCAAAAATAGTTGATCATTT 476
 XX |||||||
 XX 451 CTCTGACAGTACCTGTAACATGGAATACCGGCCAAAAATAGTTGATCATTT 510
 XX |||||||
 XX 477 CAAGATGGCATTTCCCAATGAATAACACAGTAACAT 517
 XX |||||||
 XX 511 CAAGATGGCATTTCCCAATGAATAACACAGTAACAT 551
 XX |||||||
 XX
 XX RESULT 6
 XX AAD06405
 XX ID AAD06405 standard; cDNA; 471 BP.
 XX AC
 XX AAD06405;
 XX
 XX 10-AUG-2001 (first entry)
 XX DE
 XX Rabbit liver-type IGF-I isoform (L.IGF-I) cDNA.
 XX
 XX Rabbit; IGF-I isoform; Insulin-like growth factor-I; MGF;
 XX mechano-growth factor; neurological disorder; neurodegenerative disorder;
 XX amyotrophic lateral sclerosis; spinal muscular atrophy; muscular atrophy;
 XX polymyositis; post-polio syndrome; toxin; motoneurone disorder;
 XX nerve damage; autosomal muscular dystrophy; diabetic neuropathy;
 XX sex-linked muscular dystrophy; peripheral neuropathy;
 XX Alzheimer's disease; Parkinson's disease; liver; L.IGF-I; ss.
 XX
 XX Oryctolagus cuniculus.
 XX
 XX Key Location/Qualifiers
 XX CDS 1..318
 XX /*tag= a
 XX /product= "liver-type IGF-I isoform (L.IGF-I)"
 XX /transl_except= (pos:7..9, aa:Gln)
 XX /transl_except= (pos:25..27, aa:Gln)
 XX /note= "these translation exceptions occur while decoding
 XX the alternative version of the protein (AAE02456).
 XX The CDS comprises exons 3, 4 and 6 and
 XX does not include start codon"
 XX /partial
 XX
 XX WO200136483-A1.
 XX 25-MAY-2001.
 XX 15-NOV-2000; 2000WO-GB04354.
 XX 15-NOV-1999; 99GB-0026968.
 XX (UNLO) UNIV COLLEGE LONDON.
 XX Goldslink G, Johnson I;
 XX WPI; 2001-355626/37.
 XX P-PSDB; AAE02452, AAE02456.
 XX
 XX Use of mechano-growth factor, an isoform of Insulin-like Growth
 XX Factor-I, capable of reducing motoneurone loss, in the manufacture of a
 XX medicament for the treatment of neurological disorder -
 XX
 XX Disclosure: Page 59-60; 66pp; English.
 XX
 XX The present invention relates to use of mechano-growth factor (MGF),
 XX an Insulin-like Growth Factor-I (IGF-I) isoform in the manufacture of a
 XX medicament for the treatment of neurological disorder. The MGF is capable
 XX of reducing motoneurone loss by 20% or greater in response to nerve
 XX avulsion, and effects motoneurone rescue, preferably adult motoneurone
 XX rescue. The MGF polynucleotide and polypeptide are useful in the
 XX manufacture of a medicament for the treatment of a neurological disorder.--

CC including a disorder of motoneurons and/or neurodegenerative disorder,
CC e.g., amyotrophic lateral sclerosis, spinal muscular atrophy, progressive
CC spinal muscular atrophy, infantile or juvenile muscular atrophy,
CC poliomyelitis or post-polio syndrome, a disorder caused by exposure to a
CC toxin, motoneurone trauma, a motoneurone lesion or nerve damage, an
CC injury that affects motoneurons, motoneurone loss associated with aging,
CC autosomal or sex-linked muscular dystrophy, diabetic neuropathy,
CC peripheral neuropathies, Alzheimer's disease and Parkinson's disease.
CC The present sequence is rabbit liver type IGF-1 isoform (L.IGF-1) cDNA.
CC The L.IGF-1 protein comprises amino acid sequences encoded by
CC nucleic acid sequence of IGF-1 exons 4 and 6.

50 Sequence 471 BP; 132 A; 118 C; 131 G; 90 T; 0 other;

Query Match	73.0%;	Score 377.2;	DB 22;	Length 471;
Best Local Similarity	87.8%;	Pred. No. 4.1e-104;		
Matches 455;	Conservative 0;	Mismatches 13;	Indels 50;	Gaps 2

QY 1 GGACCCGGAAGACCCTCGCGGCTGCTGAGCTGGGAGATGCTCTTACGTTGCTGCTGGAGAC 60

Db 1 GGACCCGGAAGACCCTCGCGGCTGCTGAGCTGGGAGATGCTCTTACGTTGCTGCTGGAGAC 60

QY 61 AGGAGCTTTTATTTTCAACAAGCCACAGGATATGCTCCAGACTCGAGAGCGGCTCAG 120

Db 61 AGGAGCTTTTATTTTCAACAAGCCACAGGATATGCTCCAGACTCGAGAGCGGCTCAG 120

QY 121 ACAGCATCTGGATGATGCTGCTTCGCGAGACTTGATCTAAGAGAGCTGGAGATGAT 180

Db 121 ACAGCATCTGGATGATGCTGCTTCGCGAGACTTGATCTGAGAGAGCTGGAGATGAT 180

QY 181 TCGCACAACCCTCAAGCTGCGCAAGTCAAGTCTGCTGTGCGTCCACAGCGCCACACCGAC 240

Db 181 TCGCACAACCCTCAAGCGCGGCAAGGCAAGCAGCCGCTCGCTCGTCCACAGCGCCACACCGAC 240

QY 241 ATGCCAAGACCCAGAGATATCAGCCCCCATCTACCAACAAGAACAGAGTCTCAGAGA 300

Db 241 ATGCCAAGACCTCAG----- 255

QY 301 AGGAAAGAAGTACATTTTGAAAGACACAGTAGAGGAGTGCAGAGAAACAAGAACTACAG 360

Db 256 ----AAGGAAGTACATTTTGAAAGAACACAAGTAGAGGAGTGCAGAGAAACAAGAACTACAG 311

QY 361 GATGTA-GAAGACCCTTCGAGGAGTGAAGAAAGACAGGCCACGCGAGAGCCCTTGGCTC 419

Db 312 GATGTAAGGAAGACCCTTCGAGGAGTGAAGAAAGACAGGCCACGCGAGAGCCCTTGGCTC 371

QY 420 TGCACAGTTACCTGTAAACATTTGGAATACCGGCCCCAAAATAATGATTGATCACATTTCAA 479

Db 372 TGCACAGTTACCTGTAAACATTTGGAATACCGGCCCCAAAATAATGATTGATCACATTTCAA 431

QY 480 AGATGGCATTTCCCCCAATGGAATACACAAGTAAACAT 517

Db 432 AGATGGCATTTCCCCCAATGGAATACACAAGTAAACAT 469

RESULT 7
AAS16884
ID AAS16884 standard; cDNA; 471 BP

DT 25-FEB-2002 (first entry)

DE Rabbit insulin-like growth factor I liver-type isoform (L.IGF-I) cDNA.

KW Rabbit; mechano-growth factor; insulin-like growth factor I; IGF-I; MGF;
KW neuroprotective; nerve damage; peripheral nervous system; nerve severing
KW muscle; neurological disorder; motoneuron loss; motoneuron disorder; ss;
KW nerve avulsion; insulin-like growth factor I liver-type isoform; L-IGF-I;
XX
OS *Oryctolagus cuniculus*.

FH	Key	Location/Qualifiers
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FT      CDS
FT      1..318
FT      /tag= a
FT      /product= "Rabbit L. IGF-I
FT      /partial
FT      /note= "No start codon"
FT      1..75
FT      /tag= b
FT      /number= exon 3
FT      76..258
FT      /tag= c
FT      /number= exon 4
FT      259..315
FT      /tag= d
FT      /number= exon 6

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PN	WC200185781-A2.
XX	
ED	15-NOV-2001.
XX	
PF	10-MAY-2001; 2001WO-GB02054.
XX	
PR	10-MAY-2000; 2000GB-0011278.
XX	
PA	(UNLO) UNIV COLLEGE LONDON.
EA	(HERI-) EAST GRINSTEAD MEDICAL RES TRUST

PT Use of insulin-like growth factor I (IGF-I) isoform known as mechano-growth factor which is encoded by IGF-I exons 4,5,6 and has PT ability to reduce motoneuron loss in response to nerve avulsion, to PT treat nerve damage -

PS Disclosure; Fig 10; 65pp; English.

CC The invention relates to the use of an insulin-like growth factor I
CC (IGF-I) isoform, known as mechano-growth factor (MGF), in the manufacture
CC of a medicament for treating nerve damage in the peripheral nervous
CC system, or for treating nerve damage by localising MGF at the site of
CC damage. The nerve damage may include severing of a nerve. The treatment
CC may be combined with another treatment (such as a polypeptide growth
CC factor other than MGF) that prevents or diminishes degeneration of the
CC target organ (for example, muscle) which the damaged nerve innervates,
CC whereby the treatment of the muscle with MGF or a polynucleotide encoding
CC MGF prevents or diminishes degeneration. The method is useful for
CC treating neurological disorders, preferably motoneuron disorders. These
CC methods can reduce motoneuron loss by 20% or greater in response to nerve
CC avulsion. This sequence represents cDNA encoding the rabbit insulin-like
CC growth factor I liver-type isoform (L-IGF-I) used in experiments on
CC motoneuron loss.

Sequence 471 BP; 132 A; 118 C; 131 G; 90 T; 0 other,

Query Match:	73.0%	Score 377.2:	DB 24:	Length 471:
Best Local Similarity	87.8%	Pred. No. 4.1e-104:		
Matches 455, Conservative	0:	Mismatches 13:	Indels 50:	Gaps 2:

QY	61	AGAGGCGCTTTATTTATTCACAAAGCCCAAGAGGATATGGCTCTACAGACGTGGAGGCGCCCTTCAG	120
QY		GGACCGGAGACGGCTGCGCCGGAGCTAGAGCGAGTGAATGGCTCTTCAGATTGCTGTGGAGAC	60
Db	1	GGACCGGAGACGGCTTGGCGGTGCTGAGCTGGTGGATGCTTTCAGATTGCTGTGGAGAC	60
QY		AGAGGCGCTTTATTTATTCACAAAGCCCAAGAGGATATGGCTCTACAGACGTGGAGGCGCCCTTCAG	120
Db	61	AGAGGCGCTTTATTTATTCACAAAGCCCAAGAGGATATGGCTCTACAGACGTGGAGGCGCCCTTCAG	120
QY		ACAGGCGATCGTGGAGTAGTGTGCTTCCGGAGCTGTGATCAAGAGGCTGGAGATGTAT	180
Db	121	ACAGGCGATCGTGGAGTAGTGTGCTTCCGGAGCTGTGATCAAGAGGCTGGAGATGTAT	180
QY		ACAGGCGATCGTGGAGTAGTGTGCTTCCGGAGCTGTGATCAAGAGGCTGGAGATGTAT	180
Db	121	ACAGGCGATCGTGGAGTAGTGTGCTTCCGGAGCTGTGATCAAGAGGCTGGAGATGTAT	180
QY		TGCGACCCCTCAAGCGCTGCCAAGTCAGTGCCTTGTCCGTGCCCAAGCCACACCCGAC	240
Db	181	TGCGACCCCTCAAGCGCTGCCAAGTCAGTGCCTTGTCCGTGCCCAAGCCACACCCGAC	240

Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

```

QY 1 GGACCGAGAGAGCGCTGCGGGCTGAGCTGGTGGATCTCTTACGTTGCTGTGGAGAC 60
DB 311 GGACCGAGAGAGCGCTGCGGGCTGAGCTGGTGGATCTCTTACGTTGCTGTGGAGAC 370
QY 61 AGGGGCTTTATTTCAACAGCCGACAGGATGATGCTCCAGAGTGGAGGGGCGCTCAG 120
DB 371 AGGGGCTTTATTTCAACAGCCGACAGGATGATGCTCCAGAGTGGAGGGGCGCTCAG 430
QY 121 ACAGAGCATCTGGATGATGCTGCTTCCGAGAGCTGATTAAGAGAGCTGAGATGTAT 180
DB 431 ACAGAGCATCTGGATGATGCTGCTTCCGAGAGCTGATTAAGAGAGCTGAGATGTAT 490
QY 181 TGGCACCCTCCCAAGCTGCGCAATGATGCTGCTGCTGCGCCGCGCCACACCGAC 240
DB 491 TGGCACCCTCCCAAGCTGCGCAATGATGCTGCTGCTGCGCCGCGCCACACCGAC 550
QY 241 ATGCCCCAAGACCCGAGAGATCAGCCCCCATCTAACCAAGAACAGAGTCTCAGAGA 300
DB 551 ATGCCCCAAGACCCGAGAGATCAGCCCCCATCTAACCAAGAACAGAGTCTCAGAGA 565
QY 301 AGGAAGAGAGTACATTTGAAGAACAGAGAGAGTGGAGAGAGAGAGAGAGAGAGAG 360
DB 566 ----AAGGAAGTACATTTGAAGAACAGAGAGAGTGGAGAGAGAGAGAGAGAGAG 621
QY 361 GATGTA-GAAGACCCCTTCTGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 419
DB 622 GATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 681
QY 420 TGGCAC-AGTACCTG-TAAACATTTGAGATACCGGCGCAAAATTAAGTTGATCATTTC 477
DB 682 TGGCACAGTACCTGTTAAACATTTGAGATACCGGCGCAAAATTAAGTTGATCATTTC 741
QY 478 AAGAGT-GGCATTTCCCGCAATGAATATACAGATTAACAT 517
DB 742 AAGAGTGGCGCTTCCCGCAATGAATATACAGATTAACAT 782

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RESULT 11
ABK64812
ID ABK64812 standard; DNA: 7260 BP.

AC ABK64812:
XX 18-JUN-2002 (first entry)
XX Human benign prostatic hyperplasia gene #707.
XX Human benign prostatic hyperplasia; BPH; prostate cancer; gene; ds.
XX Homo sapiens.
XX WO200212440-A2.
XX 14-FEB-2002.
XX 07-AUG-2001: 2001WO-US24708.
XX 07-AUG-2000: 2000US-223323P.
XX 05-JUN-2001: 2001US-0873319.
XX (GENE-) GENE LOGIC INC.
XX (NISB) JAPAN TOBACCO INC.
XX Munger WE, Kulhari P, Getzenberg RH, Waga I, Yamamoto J:
XX WPI: 2002-257476/30.

Identifying drugs for and diagnosing benign prostatic hyperplasia, by
PT detecting expression levels of one or more genes in prostate cells from
PT patient that are differentially regulated compared to normal prostate
PT cells

XX PS Disclosure: Page 391-393; 444pp: English.
XX CC The invention relates to a method of diagnosing (I) the onset or
XX CC progression of benign prostatic hyperplasia (BPH), or screening (II) for
XX CC or identifying an agent that modulates the onset or progression of BPH.
XX CC The method is based on changes in gene expression in BPH tissue isolated
XX CC from patients exhibiting different clinical states of prostate
XX CC hyperplasia as compared to normal prostate tissue. (I) comprises
XX CC detecting the expression levels of one or more genes in prostate cells
XX CC from the subject that are differentially regulated compared to normal
XX CC prostate cells. (II) comprises preparing a first gene expression profile
XX CC of BPH cells or BPH-like cell population, exposing the cells to the
XX CC agent, and comparing the first and second gene expression profiles.
XX CC (I) is useful for diagnosing the onset or progression of BPH. (II) is
XX CC useful for identifying an agent that modulates the onset or progression
XX CC of BPH. The methods are useful to present information identifying
XX CC the expression level in a tissue or cells, by comparing the expression
XX CC level of genes given in the specification in the tissue or cells to the
XX CC level of expression of gene in the database, and displaying the
XX CC expression levels of at least one gene in the tissue or cell sample
XX CC compared to the expression level in BPH. Agents using (II) are useful for
XX CC treating BPH or prostate cancer. ABK64105-ABK64860 represent human
XX CC benign prostatic hyperplasia gene sequences of the invention.

SQ Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other:

Query Match 66.6%; Score 344.2; DB 24; Length 7260;
Best Local Similarity 87.3%; Pred. No. 1.2e-93;
Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;

```

QY 1 GGACCGAGAGAGCGCTGCGGGCTGAGCTGGTGGATCTCTTACGTTGCTGTGGAGAC 60
DB 311 GGACCGAGAGAGCGCTGCGGGCTGAGCTGGTGGATCTCTTACGTTGCTGTGGAGAC 370
QY 61 AGGGGCTTTATTTCAACAGCCGACAGGATGATGCTCCAGAGTGGAGGGGCGCTCAG 120
DB 371 AGGGGCTTTATTTCAACAGCCGACAGGATGATGCTCCAGAGTGGAGGGGCGCTCAG 430
QY 121 ACAGAGCATCTGGATGATGCTGCTTCCGAGAGCTGATTAAGAGAGCTGAGATGTAT 180
DB 431 ACAGAGCATCTGGATGATGCTGCTTCCGAGAGCTGATTAAGAGAGCTGAGATGTAT 490
QY 181 TGGCACCCTCCCAAGCTGCGCAATGATGCTGCTGCTGCGCCGCGCCACACCGAC 240
DB 491 TGGCACCCTCCCAAGCTGCGCAATGATGCTGCTGCTGCGCCGCGCCACACCGAC 550
QY 241 ATGCCCCAAGACCCGAGAGATCAGCCCCCATCTAACCAAGAACAGAGTCTCAGAGA 300
DB 551 ATGCCCCAAGACCCGAGAGATCAGCCCCCATCTAACCAAGAACAGAGTCTCAGAGA 565
QY 301 AGGAAGAGAGTACATTTGAAGAACAGAGAGAGTGGAGAGAGAGAGAGAGAGAGAG 360
DB 566 ----AAGGAAGTACATTTGAAGAACAGAGAGAGTGGAGAGAGAGAGAGAGAGAG 621
QY 361 GATGTA-GAAGACCCCTTCTGAGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAG 419
DB 622 GATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 681
QY 420 TGGCAC-AGTACCTG-TAAACATTTGAGATACCGGCGCAAAATTAAGTTGATCATTTC 477
DB 682 TGGCACAGTACCTGTTAAACATTTGAGATACCGGCGCAAAATTAAGTTGATCATTTC 741
QY 478 AAGAGT-GGCATTTCCCGCAATGAATATACAGATTAACAT 517
DB 742 AAGAGTGGCGCTTCCCGCAATGAATATACAGATTAACAT 782

```

RESULT 12
ABK35504
ID ABK35504 standard; DNA: 7260 BP.

AC ABR35504;
 XX
 DT 08-MAY-2002 (first entry)
 DE Human endometrial cancer related gene, IGFI.
 XX Human endometrial cancer; differential expression;
 XX Human ds; gene: endometrial cancer; differential expression;
 KM DNA microarray; protein microarray.
 XX
 OS Homo sapiens.
 PN WO200209573-A2.
 PD 07-FEB-2002.
 PF 31-JUL-2001: 2001WO-US24104.
 PR 31-JUL-2000: 2000US-221735P.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 PI Mutter GL;
 DR WPI: 2002-179967/23.
 DR P-PSDB: AA084284.
 XX
 PT Diagnosing endometrial cancer comprises determining expression of
 PT nucleic acid molecules or expression products that are differentially
 PT expressed in normal and malignant endometrium -
 PS Claim 1: Page 85-89; 233pp; English.
 XX
 CC The invention relates to diagnosing endometrial cancer in a subject
 CC suspected of having endometrial cancer comprising determining the
 CC expression of a set of nucleic acid molecules or expression products in
 CC an endometrial sample suspected of being cancerous, where the set of
 CC nucleic acid molecules comprises at least 2 nucleic acid molecules
 CC selected from 50 fully defined sequences as given in the specification.
 CC The nucleic acids are used as an array of at least 2 of the 50
 CC nucleic acids bound to a solid substrate. Also included is a solid-phase
 CC protein microarray comprising at least 2 antibodies or its antigen
 CC binding fragments, that specifically bind at least 2 different
 CC polypeptides from the 50 fully defined sequences as given in the
 CC specification, fixed to a solid substrate. The methods and arrays are
 CC useful for the diagnosis of endometrial cancer, selecting and monitoring
 CC treatment regimens and identification of lead compounds useful for the
 CC treatment of endometrial cancer. The present sequence is one of 50
 CC genes differentially expressed between cancerous and non-cancerous
 CC samples.
 SO Sequence 7260 BP; 2330 A; 1415 C; 1240 G; 2275 T; 0 other:
 Query Match 66.6%; Score 344.2; DB 24; Length 7260;
 Best Local Similarity 87.3%; Pred. No. 1.2e-93;
 Matches 455; Conservative 0; Mismatches 13; Indels 53; Gaps 5;
 1 GGACCGAGACGCTGCGGGCTGAGCTGTGATGCTCTCAGTCTGTGTGAGAC 60
 311 GGACCGAGACGCTGCGGGCTGAGCTGTGATGCTCTCAGTCTGTGTGAGAC 370
 61 AGGCGCTTTTATTCAACAAGCCACAGGGTATGGCTCAGCAGTGGAGGGCGCTCAG 120
 371 AGGCGCTTTTATTCAACAAGCCACAGGGTATGGCTCAGCAGTGGAGGGCGCTCAG 430
 121 ACAGGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 431 ACAGGATGTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 490
 181 TGGCAGCCCTCAAGCTCCAGAGTCAAGTCTGTCTGTCTGTCTGTCTGTCTGTCT 240
 491 TGGCAGCCCTCAAGCTCCAGAGTCAAGTCTGTCTGTCTGTCTGTCTGTCTGTCT 550
 241 ATGCCCAAGACCAAGATATGAGCCCATCTACCAACAAGACGAGTCTCAGAGA 300

DB 551 ATGCCCAAGACCCAG----- 565
 QY 301 AGGAAGCAAGTACATTGTAAGACACACACTAGAGGAGTGCAGGAACAAGACTACAG 360
 DB 566 ---AAGGAAGTACATTGTAAGACACACACTAGAGGAGTGCAGGAACAAGACTACAG 621
 QY 361 GATGTA-GAAGACCTCTGTAGAGTGAAGAGACAGCCACCGCAGACCTTGTCTC 419
 DB 622 GATCTAGGAAGACCTCTGTAGAGTGAAGAGACAGCCACCGCAGACCTTGTCTC 681
 QY 420 TGCAC-AGTTACCTG-TAAACATTGGAATACCGGCCAAAAAATAGTTGATCACTTTC 477
 DB 682 TGCACAGATTACCTGTTAACTTTGGAACACCTACAAAAAATAGTTGATCACTTTC 741
 QY 478 AAGAT-GGCATTTCCCAATGAATACACAGTAACAT 517
 DB 742 AAGATGGCGTTTCCCAATGAATACACAGTAACAT 782
 RESULT 13
 ABR35561
 ID ABR35561 standard; DNA; 7260 BP.
 AC ABR35561;
 XX
 DT 08-MAY-2002 (first entry)
 DE Gene IGFI differentially expressed in breast cancer tissue.
 XX
 KM Human; diagnosis of breast cancer; endometrial cancer; breast tumour;
 KM MAI; mitotic activity index; cytostatic; gene; ds.
 XX
 OS Homo sapiens.
 PN WO200210436-A2.
 PD 07-FEB-2002.
 PF 27-JUL-2001: 2001WO-US33642.
 PR 28-JUL-2000: 2000US-222093P.
 PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
 PI Mutter GL;
 DR WPI: 2002-180084/23.
 DR P-PSDB: AA084341.
 XX
 PT Diagnosing breast cancer comprises determining expression of nucleic
 PT acid molecules or expression products that are differentially expressed
 PT in normal and malignant tissue -
 PS Claim 1: Page 74-78; 219pp; English.
 XX
 CC The present invention relates to a method for diagnosing breast cancer
 CC in a subject suspected of having endometrial cancer. The method
 CC comprises determining the expression of a set of human genes or
 CC expression products in an endometrial sample suspected of being
 CC cancerous. The human genes of the invention are differentially
 CC expressed in breast tumours characterised as high or low MAI (mitotic
 CC activity index). These sets of genes can be used to discriminate between
 CC high and low MAI breast tumours. The invention also provides DNA and
 CC protein microarrays for analysing the expression of the human genes and
 CC their protein products. The methods and arrays are useful for the
 CC diagnosis and prognosis of endometrial cancer, selecting and monitoring
 CC treatment regimens, and identification of compounds useful for the
 CC treatment of endometrial cancer. ABR35531-ABR35581 represent the human
 CC genes of the invention that are differentially expressed in breast
 CC cancer tissue.

XX 03-OCT-2002 (updated)
 DT 31-JUL-1991 (first entry)
 XX Human prepro-somatomedin-C.
 DE Somatomedin-C; ss.
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FT CDS 3..360
 FT /*tag= a
 FT /label= prepro-somatomedin-C
 FT mat_peptide 45..254
 FT /*tag= b
 FT /label= mature somatomedin-C
 XX
 XX W08600619-A.
 XX 30-JAN-1986.
 XX
 XX 10-JUL-1985: 85WO-US01325.
 XX
 XX 13-JUL-1984: 84US-0630557.
 XX
 XX (CHIR-) CHIRON CORP.
 XX
 XX Bell G, Rail LB, Merryweather JP;
 XX WPI: 1986-042104/05.
 XX P-PSDB: AAP60578.
 XX
 XX Pre:pro insulin-like growth factors I and II - obt'd. from the
 XX human genome by e.g. screening a cDNA library obt'd. from human
 XX liver cells.
 XX
 XX PS Disclosure: Fig 1: 20pp; English.
 XX
 XX The sequence, derived from plasmid phage phigfl, encodes human
 XX prepro-somatomedin-C. The sequence may be used for hormone
 XX production, and is useful for the preparation of DNA probes to
 XX detect the presence of the genes in a natural source. The probes
 XX may be used to detect mutations and/or deletions in humans
 XX suffering from growth deficiencies.
 XX See also AA060489, AA060491
 XX (Updated on 03-OCT-2002 to add missing OS field.)
 XX
 XX SQ Sequence 522 BP: 171 A; 147 C; 161 G; 143 U; 0 other;
 XX
 XX Query Match 65.6%; Score 339.4; DB 7; Length 622;
 XX Best Local Similarity 69.7%; Pred. No. 1.3e-92;
 XX Matches 363; Conservative 89; Mismatches 16; Indels 53; Gaps 5;
 QY 1 GGACCGAGAGCGCTGCGGGGCTGAGCTGATGCTCTCAGTCTGCTGTGAGAGC 60
 Db 45 GGACCGAGAGCGCTGCGGGGCTGAGCTGATGCTCTCAGTCTGCTGTGAGAGC 104
 QY 61 AGGGGCTTTATTCAACAAGCCCAAGGGTATGCTCCAGAGTGGAGGGCCCTCAG 120
 Db 105 AGGGGCTTTATTCAACAAGCCCAAGGGTATGCTCCAGAGTGGAGGGCCCTCAG 164
 QY 121 ACAGGATCGTGTAGTGTCTGCTCCGAGCTGTGATCTAAGAGGCTGAGATGTAT 180
 Db 165 ACAGGATCGTGTAGTGTCTGCTCCGAGCTGTGATCTAAGAGGCTGAGATGTAT 224
 QY 181 TCGGCAACCCCTCAAGCTGCGCAAGTACGCTGCTGTCCGTCACAGCCGACGAC 240
 Db 225 TCGGCAACCCCTCAAGCTGCGCAAGTACGCTGCTGTCCGTCACAGCCGACGAC 284
 QY 241 ATGCCCAAGACCAAGATATGAGCCCATCTACCAACAAGACGAAAGTCTCAGAGA 300
 Db 285 ATGCCCAAGACCAAGATATGAGCCCATCTACCAACAAGACGAAAGTCTCAGAGA 299

QY 301 AGGAAGAGAGTACATTTGAAGAACACAGTAGAGGGAGTGCAGAGAAACAAGAACTACG 360
 Db 300 ----AAGGAAGUACAUUUGAAGAACGCAAGUGAGGGAGUGGACAGAAACAAGAACTACG 355
 QY 361 GATGTA-GAAGACCCCTTCTGAGAGTGAAGAAAGACAGCCGACGCGAGACCTTGTCTC 419
 Db 356 GAUGUAGAGAACACCCCTTCTGAGAGTGAAGAAAGACAGCCGACGCGAGACCTTGTCTC 415
 QY 420 TGCAC-AGTACCTG-TAAGCATTTGGAAATACCGGCCCAAAAAATAGTTGATCATTTC 477
 Db 416 UGCACGAGUUAACUUGUUAACUUGUUAACUUGUUAACUUGUUAACUUGUUAACUUGUUA 475
 QY 478 AAGAT-GGCATTTCCCGCAATGAATACACAACTAAACAT 517
 Db 476 AAGATGGGCGUUDCCCGCAATGAATACACAACTAAACAT 516

Search completed: June 15, 2003, 16:08:47
 Job time : 160.835 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2003 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 15:46:38 ; Search time 41.9101 Seconds
(without alignments)
3783.145 Million cell updates/sec

Title: US-09-852-261-1

Perfect score: 517

Sequence: 1 ggaacgagagcgtctgcg.....tgaatcacacaagaataacat 517

Scoring table: IDENTITY_NUC

Searched: 441362 seqs, 15338381 residues

Total number of hits satisfying chosen parameters: 882724

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : Issued Patents NA:*

- 1: /cgn2_6/prodata/2/ina/58_COMB.seq:*
- 2: /cgn2_6/prodata/2/ina/58_COMB.seq:*
- 3: /cgn2_6/prodata/2/ina/58_COMB.seq:*
- 4: /cgn2_6/prodata/2/ina/58_COMB.seq:*
- 5: /cgn2_6/prodata/2/ina/58_COMB.seq:*
- 6: /cgn2_6/prodata/2/ina/58_COMB.seq:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	467.4	90.4	553	4	US-09-142-583A-3
2	467.4	90.4	553	4	US-09-142-583A-5
3	342.6	66.3	777	4	US-09-142-583A-10
4	339.4	65.6	622	6	5405942-2
5	286.4	55.4	5707	2	US-08-472-809B-8
6	286.4	55.4	6345	2	US-08-472-809B-7
7	255.2	45.4	357	6	5405942-13
8	253.6	49.1	357	6	5405942-9
9	208.4	40.3	210	6	5405942-7
10	208.4	40.3	210	6	5405942-11
11	208.4	40.3	2862	4	US-09-255-829-13
12	206.8	40.0	210	6	5405942-15
13	202.8	39.2	240	6	US-08-308-196A-1
14	202.8	39.2	240	5	PCT-US91-06452-1
15	202.8	39.2	390	3	US-09-029-267-13
16	174.4	33.7	798	1	US-07-953-230A-6
17	163.4	31.6	770	1	US-07-953-230A-1
18	163.4	31.6	846	1	US-07-953-230A-5
19	125.8	24.3	485	1	US-07-989-845-29
20	125.8	24.3	485	1	US-07-989-844-13
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22	125.8	24.3	485	1	US-08-169-688-1
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25	125.8	24.3	485	1	US-08-110-664-1
26	125.8	24.3	485	1	US-08-446-882-1
27	125.8	24.3	485	1	US-08-385-187A-1

28	125.8	24.3	485	1	US-08-470-108-1	Sequence 1, Appl
29	125.8	24.3	485	5	PCT-US93-11287-13	Sequence 13, Appl
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31	123.8	23.9	621	3	US-08-989-251-40	Sequence 40, Appl
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33	123.8	23.9	621	3	US-09-528-108-40	Sequence 40, Appl
34	122	23.6	237	1	US-07-764-655D-8	Sequence 75, Appl
35	120.8	23.3	233	2	US-08-482-183-75	Sequence 3, Appl
36	120.4	23.3	233	1	US-08-444-143-3	Sequence 3, Appl
37	120.4	23.3	233	1	US-07-764-655D-9	Sequence 9, Appl
38	120.4	23.3	237	1	US-08-284-784-40	Sequence 40, Appl
39	120.4	23.3	717	2	US-08-854-811-40	Sequence 43, Appl
40	120.4	23.3	783	2	US-08-284-784-43	Sequence 43, Appl
41	120.4	23.3	783	2	US-08-854-811-43	Sequence 33, Appl
42	120.4	23.3	891	1	US-08-284-784-34	Sequence 34, Appl
43	120.4	23.3	891	2	US-08-854-811-33	Sequence 33, Appl
44	120.4	23.3	891	2	US-08-854-811-33	Sequence 33, Appl
45	120.4	23.3	891	2	US-08-854-811-33	Sequence 33, Appl

ALIGNMENTS

RESULT 1
US-09-142-583A-3
Sequence 3, Application US/09142583A
Patent No. 6221842
GENERAL INFORMATION:
APPLICANT: GOLDSPIK, GEFREY
TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentio Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/142,583A
FILING DATE: 29-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB97/00658
FILING DATE: 11-MAR-1997
APPLICATION NUMBER: GB 9605124.8
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36663
REFERENCE/DOCKET NUMBER: 117-263
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 553 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 1..363
SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-142-583A-3
Query Match 90.4%; Score 467.4; DB 4; Length 553;

Best Local Similarity 96.2%; Pred. No. 1.2e-134;
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

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DB 31 GGACCGGAGACGCTGCGGGGCTAGCTGCTGCTCTTCACTTCTGTGTGGAGAC 90
QY 61 AGGGGCTTTTATTCAACAGAGCCGACAGGATGCTCCAGAGTCCGAGGCGCCCTCAG 120
DB 91 AGGGGCTTTTATTCAACAGAGCCGACAGGATGCTCCAGAGTCCGAGGCGCCCTCAG 150
QY 121 ACAGGCTATGCTGATGCTGCTCTTCCGAGGCTGTGATCTAGAGGCTGAGATGTAT 180
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DB 271 ATGCCAAGACCCAGAGTATCAGCCCTCATCTACCAAGAGAGAAATGATCTCAGAG 330
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DB 331 AGAAGGAAAGGAGTACATTTGAGAGACAAAGTGAAGGAGTGCAGAGAAACAACTA 390
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DB 391 CAGATGTAAGAGAGACCTCTGAGAGAGTGAAGAGAGACAGCCAGACCTTTG 450
QY 417 CTCTGACAGTACTCTGTAACATTTGAAATCCGCGCCAAAATTAAGTTGATACATTT 476
DB 451 CTCTGACAGTACTCTGTAACATTTGAAATCCGCGCCAAAATTAAGTTGATACATTT 510
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RESULT 2

US-09-142-583A-5
Sequence 5, Application US/09142583A
Patent No. 6221842

GENERAL INFORMATION:

APPLICANT: GOLDSPIRK, GEOFFREY
TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.25
CURRENT APPLICATION NUMBER: US/09/142,583A
FILING DATE: 29-Oct-1998
CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: WO PCT/GB97/00658
FILING DATE: 11-MAR-1997
APPLICATION NUMBER: GB 9605124.8
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36663
REFERENCE/DOCKET NUMBER: 11-263

TELECOMMUNICATION INFORMATION:

TELEPHONE: 7038164000
TELEFAX: 7038164100

INFORMATION FOR SEQ ID NO: 5:

SEQUENCE CHARACTERISTICS:
LENGTH: 553 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: Linear
MOLECULE TYPE: cDNA
FEATURE:

NAME/KEY: CDS
LOCATION: 341..397

US-09-142-583A-5
SEQUENCE DESCRIPTION: SEQ ID NO: 5:

Query Match 90.4%; Score 467.4; DB 4; Length 553;
Best Local Similarity 96.2%; Pred. No. 1.2e-134;
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

QY 1 GGACCGGAGACGCTGCGGGGCTAGCTGCTGCTCTTCACTTCTGTGTGGAGAC 60
DB 31 GGACCGGAGACGCTGCGGGGCTAGCTGCTGCTCTTCACTTCTGTGTGGAGAC 90
QY 61 AGGGGCTTTTATTCAACAGAGCCGACAGGATGCTCCAGAGTCCGAGGCGCCCTCAG 120
DB 91 AGGGGCTTTTATTCAACAGAGCCGACAGGATGCTCCAGAGTCCGAGGCGCCCTCAG 150
QY 121 ACAGGCTATGCTGATGCTGCTCTTCCGAGGCTGTGATCTAGAGGCTGAGATGTAT 180
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DB 271 ATGCCAAGACCCAGAGTATCAGCCCTCATCTACCAAGAGAGAAATGATCTCAGAG 330
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DB 331 AGAAGGAAAGGAGTACATTTGAGAGACAAAGTGAAGGAGTGCAGAGAAACAACTA 390
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QY 417 CTCTGACAGTACTCTGTAACATTTGAAATCCGCGCCAAAATTAAGTTGATACATTT 476
DB 451 CTCTGACAGTACTCTGTAACATTTGAAATCCGCGCCAAAATTAAGTTGATACATTT 510
QY 477 CAAGATGCAATTTCCCAATGAATACAAAGTAACAT 517
DB 511 CAAGATGCAATTTCCCAATGAATACAAAGTAACAT 551

RESULT 3

US-09-142-583A-10
Sequence 10, Application US/09142583A
Patent No. 6221842

GENERAL INFORMATION:

APPLICANT: GOLDSPIRK, GEOFFREY
TITLE OF INVENTION: METHOD OF TREATING MUSCULAR DISORDERS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE P.C.
STREET: 1100 NORTH GLEBE ROAD
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/142,583A
FILING DATE: 29-Oct-1998
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/GB97/00658
FILING DATE: 11-MAR-1997
APPLICATION NUMBER: GB 9605124.8
FILING DATE: 11-MAR-1996
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B. J.
REGISTRATION NUMBER: 36663
REFERENCE/DOCKET NUMBER: 117-263
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 777 base pairs
TYPE: nucleic acid
STRANDEDNESS: both
TOPOLOGY: linear
MOLECULE TYPE: cDNA
FEATURE:
NAME/KEY: CDS
LOCATION: 26..493
SEQUENCE DESCRIPTION: SEQ ID NO: 10:
US-09-142-583A-10

Query Match 66.3%; Score 342.6; DB 4; Length 777;
Best Local Similarity 87.1%; Pred. No. 3.8e-96;
Matches 454; Conservative 0; Mismatches 14; Indels 53; Gaps 5;

1 GGACCGGAGAGCGCTCGGGGCTGAGCTGATGATCTCTTCAGTTCGTTGAGGAGAC 60
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301 AGGAAGAAGATGATTTGAAGAACAAGTAGAGGAGTGCAGAAACAGAACTACAG 360
434 ----AAGGAAGTACATTTGAAGAACAAGTAGAGGAGTGCAGAAACAGAACTACAG 489
361 GATGTA-GAAGACCCCTCTGAGAGTGAAGAGACAGGCCAGCCGAGACCTTTGCTC 419
490 GATGTAAGAGAGCCCTCTGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 549
420 TGCAAC-AGTACCTG-TAAGCATTTGGAATACCGGCAAAATTAAGTTGATACATTTTC 477
550 TGCAACAGTACCTGTTAACTTTGGAAGACCTACCAAAAAATTAAGTTGATACATTTTA 609
478 AAGGAT-GGCAATTTCCCAATGAATATACCAAGTAAACAT 517
610 AAGGATGGCGTTCCCAATGAATATACCAAGTAAACAT 650

RESULT 4
5405942-2
Patent No. 5405942
APPLICANT: BELT, GRAEME I.; FALL, LESLIE B.; MERRYWEATHER,
JAMES P.
TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
I AND II
NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/65,673
FILING DATE: 16-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 630,557
FILING DATE: 19-JUL-1984
SEQ ID NO: 2
LENGTH: 622

Query Match 65.6%; Score 339.4; DB 6; Length 622;
Best Local Similarity 69.7%; Pred. No. 3.4e-95;
Matches 363; Conservative 89; Mismatches 16; Indels 53; Gaps 5;

1 GGACCGGAGAGCGCTCGGGGCTGAGCTGATGATCTCTTCAGTTCGTTGAGGAGAC 60
45 GGACCGGAGAGCGCTCGGGGCTGAGCTGATGATCTCTTCAGTTCGTTGAGGAGAC 104
61 AGGGGCTTTTATTTCACAAGCCCAAGGATATGCTCCAGAGTCGAGGCGCCCTCAG 120
105 AGGGGCTTTTATTTCACAAGCCCAAGGATATGCTCCAGAGTCGAGGCGCCCTCAG 164
121 ACAGGATCGTGATGATGCTGCTGCTCCGAGCTGATATAGAGAGCTGGAGATGAT 180
165 ACAGGATCGTGATGATGCTGCTGCTCCGAGCTGATATAGAGAGCTGGAGATGAT 224
181 TGCGCACCCCTCAAGCCTGCGCAAGTCAGCTGCTGCTCCGAGCTGATATAGAGAG 240
225 TGCGCACCCCTCAAGCCTGCGCAAGTCAGCTGCTGCTCCGAGCTGATATAGAGAG 284
241 ATGCGCCAGAGCCGAGAGTATCAAGCCCTCTTACCAACAGAACAGAAAGTCTCAGAGA 300
285 ATGCGCCAGAGCCGAGAGTATCAAGCCCTCTTACCAACAGAACAGAAAGTCTCAGAGA 299
301 AGGAAGAAGATGATTTGAAGAACAAGTAGAGGAGTGCAGAAACAGAACTACAG 360
300 ----AAGGAAGTACATTTGAAGAACAAGTAGAGGAGTGCAGAAACAGAACTACAG 355
361 GATGTA-GAAGACCCCTCTGAGAGTGAAGAGACAGGCCAGCCGAGACCTTTGCTC 419
356 GAUGUAGAGAGACCCCTCTGAGAGTGAAGAGACAGGCCAGCCGAGACCTTTGCTC 415
420 TGCAAC-AGTACCTG-TAAGCATTTGGAATACCGGCAAAATTAAGTTGATACATTTTC 477
416 UGCACAGAGUACCCCTGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAG 475
478 AAGGAT-GGCAATTTCCCAATGAATATACCAAGTAAACAT 517
476 AAGGATGGCGTTCCCAATGAATATACCAAGTAAACAT 516

RESULT 5
US-08-472-809B-8
Sequence 8, Application US/08472809B
Patent No. 5925564
GENERAL INFORMATION:
APPLICANT: Schwartz, Robert J.
APPLICANT: DeMayo, Franco J.
APPLICANT: O'Malley, Bert W.
TITLE OF INVENTION: Expression Vector Systems and
METHOD OF INVENTION: Method of use
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSER: Lyon & Lyon

```

STREET: 633 West Fifth Street
STREET: Suite 4700
City: Los Angeles
STATE: California
COUNTRY: U.S.A.
ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,809B
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/209,846
FILING DATE: March 9, 1994
APPLICATION NUMBER: 07/789,919
FILING DATE: No. 5925564ember 6, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Marburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 214/212
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ. ID NO: 8
SEQUENCE CHARACTERISTICS:
LENGTH: 5707 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-472-809B-8

Query Match      55.4%; Score 286.4; DB 2; Length 5707;
Best Local Similarity 85.6%; Pred. No. 1.9e-78;
Matches 363; Conservative 0; Mismatches 11; Indels 50; Gaps 2;

1  GGACCGGAGAGCGCTGCGGGGCGTGAAGTGGATGCTCTCAGTGTGTGGAGAC 60
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Db  793  GGACCGGAGAGCGCTGCGGGGCGTGAAGTGGATGCTCTCAGTGTGTGGAGAC 852
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QY  61  AGGGGCTTTATTTCACAAAGCCACAGGGTATGGCTCCAGCAGTCCGAGGCGCCTCAG 120
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Db  853  AGGGGCTTTATTTCACAAAGCCACAGGGTATGGCTCCAGCAGTCCGAGGCGCCTCAG 912
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QY  121  ACAGGATGCTGATAGTGTGCTGCTCCGAGCTGTGATCTAAGAGGCTGAGATGAT 180
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Db  913  ACAGGATGCTGATAGTGTGCTGCTCCGAGCTGTGATCTAAGAGGCTGAGATGAT 972
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QY  181  TGGGCAACCCCTCAAGGCTGCCAAGTCAAGCTGCTGTGCCAGGCCACACCGAC 240
    |||||||
Db  973  TGGGCAACCCCTCAAGGCTGCCAAGTCAAGCTGCTGTGCCAGGCCACACCGAC 1032
    |||||||

QY  241  ATGCCCAAGACCCAGAGTATCAGCCCCCATCTACCAACAAGACCAAGTCTCAGAGA 300
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Db  1033  ATGCCCAAGACCCAG----- 1047
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QY  301  AGGAAGAGATGATTTGAAGACAGAGTAGAGAGTGCAGAAACAAGATACAG 360
    |||||||
Db  1048  ----AGGAAGATGATTTGAAGACAGAGTAGAGAGTGCAGAAACAAGATACAG 1103
    |||||||

QY  361  GATGTA-GAAGACCTTTGAGAGAGTGAAGAAGACAGGCCACCGAGAGCCCTTGTCTC 419
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Db  1104  GATGTAAGAGAGACCTTCTCAGAGAGTGAAGAAGATGATGACACCGAGAGATCCCGCGGAC 1163
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Db  1164  TGCA 1167

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RESULT 6
US-08-472-809B-7
; Sequence 7, Application US/08472809B
; Patent No. 5925564
; GENERAL INFORMATION:
; APPLICANT: Schwartz, Robert J.
; APPLICANT: Demayo, Franco J.
; APPLICANT: O'Malley, Bert W.
; TITLE OF INVENTION: Expression Vector Systems and
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Lyon & Lyon
; STREET: 633 West Fifth Street
; STREET: Suite 4700
; CITY: Los Angeles
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 90071-2066
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/472,809B
FILING DATE: June 7, 1995
CLASSIFICATION: 435
PRIORITY APPLICATION DATA:
APPLICATION NUMBER: 08/209,846
FILING DATE: March 9, 1994
APPLICATION NUMBER: 07/789,919
FILING DATE: No. 5925564ember 6, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Marburg, Richard J.
REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 214/212
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ. ID NO: 7
SEQUENCE CHARACTERISTICS:
LENGTH: 6345 bases
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
US-08-472-809B-7

Query Match      55.4%; Score 286.4; DB 2; Length 6345;
Best Local Similarity 85.6%; Pred. No. 2e-78;
Matches 363; Conservative 0; Mismatches 11; Indels 50; Gaps 2;

1  GGACCGGAGAGCGCTGCGGGGCGTGAAGTGGATGCTCTCAGTGTGTGGAGAC 60
    |||||||
Db  3702  GGACCGGAGAGCGCTGCGGGGCGTGAAGTGGATGCTCTCAGTGTGTGGAGAC 3761
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QY  61  AGGGGCTTTATTTCACAAAGCCACAGGGTATGGCTCCAGCAGTCCGAGGCGCCTCAG 120
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Db  3762  AGGGGCTTTATTTCACAAAGCCACAGGGTATGGCTCCAGCAGTCCGAGGCGCCTCAG 3821
    |||||||

QY  121  ACAGGATGCTGATAGTGTGCTGCTCCGAGCTGTGATCTAAGAGGCTGAGATGAT 180
    |||||||
Db  3822  ACAGGATGCTGATAGTGTGCTGCTCCGAGCTGTGATCTAAGAGGCTGAGATGAT 3881
    |||||||

QY  181  TGGCACCCTTCAGGCTGCCAAGTCAAGTCAAGCTGCTGTGCCAGGCCACACCGAC 240
    |||||||
Db  3882  TGGCACCCTTCAGGCTGCCAAGTCAAGTCAAGCTGCTGTGCCAGGCCACACCGAC 3941

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JAMES P.
TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
I AND II
NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/65,673
FILING DATE: 16-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 630,557
FILING DATE: 19-JUL-1984
SEQ ID NO:11
LENGTH: 210

Query Match 40.3%; Score 208.4; DB 6; Length 210;
Best Local Similarity 99.5%; Pred. No. 4.8e-55;
Matches 209; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGACCGGAGAGCGCTCTGCGGGCTGAGCTGGATGCTCTTCAATTGCTGTGTGAGAC 60
DB 1 GGACCGGAGAGCGCTCTGCGGGCTGAGCTGGATGCTCTTCAATTGCTGTGTGAGAC 60
QY 61 AGGGGCTTTTATTCAACAAGCCACAGGGTATGCTCCAGCAGTCGAGGGCGCTCAG 120
DB 61 AGGGGCTTTTATTCAACAAGCCACAGGGTATGCTCCAGCAGTCGAGGGCGCTCAG 120
QY 121 ACAGCATGCTGATGATGCTGCTCTCCGAGGCTGTATCTAAGAGGCTGAGATGAT 180
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QY 181 TGCGCACCCCTCAAGCTGCGCAAGTCAGCT 210
DB 181 TGCGCACCCCTCAAGCTGCGCAAGTCAGCT 210

RESULT 11
US-09-829-13
Sequence 13, Application US/09255829
Patent No. 6461617
GENERAL INFORMATION:
APPLICANT: Shone, Clifford Charles
APPLICANT: Quinn, Conrad Padraig
APPLICANT: Foster, Keith Alan
TITLE OF INVENTION: Recombinant Toxin Fragments
NUMBER OF SEQUENCES: 29
CORRESPONDENCE ADDRESS:
ADDRESSEE: STERN, KESSLER, GOLDSTEIN, & FOX P.L.L.C.
STREET: 1100 NEW YORK AVENUE, NW, SUITE 600
CITY: WASHINGTON
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/255,829
FILING DATE: 23-FEB-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB97/02273
FILING DATE: 22-AUG-1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/782,893
FILING DATE: 27-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: ESMOND, ROBERT W.
REGISTRATION NUMBER: 32,893
REFERENCE/DOCKET NUMBER: 1581.0130002
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
TELEFAX: 202-371-2540

INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 2862 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
NAME/KEY: CDS
LOCATION: 1..2862
US-09-829-13

Query Match 40.3%; Score 208.4; DB 4; Length 2862;
Best Local Similarity 99.5%; Pred. No. 1.5e-54;
Matches 209; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 GGACCGGAGAGCGCTCTGCGGGCTGAGCTGGATGCTCTTCAATTGCTGTGTGAGAC 60
DB 2644 GGACCGGAGAGCGCTCTGCGGGCTGAGCTGGATGCTCTTCAATTGCTGTGTGAGAC 2703
QY 61 AGGGGCTTTTATTCAACAAGCCACAGGGTATGCTCCAGCAGTCGAGGGCGCTCAG 120
DB 2704 AGGGGCTTTTATTCAACAAGCCACAGGGTATGCTCCAGCAGTCGAGGGCGCTCAG 2763
QY 121 ACAGCATGCTGATGATGCTGCTCTCCGAGGCTGTATCTAAGAGGCTGAGATGAT 180
DB 2764 ACAGCATGCTGATGATGCTGCTCTCCGAGGCTGTATCTAAGAGGCTGAGATGAT 2823
QY 181 TGCGCACCCCTCAAGCTGCGCAAGTCAGCT 210
DB 2824 TGCGCACCCCTCAAGCTGCGCAAGTCAGCT 2853

RESULT 12
US-09-829-15
Patent No. 5405942
APPLICANT: BELL, GRAEME I.; RALL, LESLIE B.; MERRYWEATHER,
JAMES P.
TITLE OF INVENTION: PREPRO INSULIN-LIKE GROWTH FACTORS
I AND II
NUMBER OF SEQUENCES: 16
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/65,673
FILING DATE: 16-JUN-1987
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 630,557
FILING DATE: 19-JUL-1984
SEQ ID NO:15
LENGTH: 210

Query Match 40.0%; Score 206.8; DB 6; Length 210;
Best Local Similarity 77.1%; Pred. No. 1.5e-54;
Matches 162; Conservative 46; Mismatches 2; Indels 0; Gaps 0;

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DB 1 GGACCGGAGAGCGCTCTGCGGGCTGAGCTGGATGCTCTTCAATTGCTGTGTGAGAC 60
QY 61 AGGGGCTTTTATTCAACAAGCCACAGGGTATGCTCCAGCAGTCGAGGGCGCTCAG 120
DB 61 AGGGGCTTTTATTCAACAAGCCACAGGGTATGCTCCAGCAGTCGAGGGCGCTCAG 120
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QY 181 TGCGCACCCCTCAAGCTGCGCAAGTCAGCT 210
DB 181 TGCGCACCCCTCAAGCTGCGCAAGTCAGCT 210

RESULT 13

Sequence 13: Application US/09029267
Patent No. 6107057
GENERAL INFORMATION:
APPLICANT: Crawford, Kenneth
APPLICANT: Zaror, Isabel
APPLICANT: Innis, Michael
TITLE OF INVENTION: Pichia Secretary Leader for Protein
TITLE OF INVENTION: Expression
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: United States
ZIP: 94608
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/029,267
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Chung, Ling-Fong
REGISTRATION NUMBER: 36,482
REFERENCE/DOCKET NUMBER: 1165.100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2704
TELEFAX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic"
US-09-029-267-13

Query Match 39.2% Score 202.8; DB 3; Length 390;
Best Local Similarity 96.7%; Pred. No. 3.3e-53;
Matches 207; Conservative 0; Mismatches 7; Indels 0; Gaps 0;
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DB 160 GGACCGAGAGCGCTCTGCGGGGCTGAGCTGTGATGCTCTTCAGTTCGTGTGTGAGAC 219
QY 61 AGGGGCTTTTATTTCACACAGGCCACAGGGTATGCTCCAGCAGTCGGAGGGCGCTCAG 120
DB 220 AGGGGCTTTTATTTCACACAGGCCACAGGGTATGCTCCAGCAGTCGGAGGGCGCTCAG 279
QY 121 ACAGGATGATGATGATGATGCTCTCCGAGCTGTATTAAGAGAGCTGAGATGTAT 180
DB 280 ACAGGATGATGATGATGATGCTCTCCGAGCTGTATTAAGAGAGCTGAGATGTAT 339
QY 181 TCGCAGACCCCTCAAGCCTGCGAAGTCAGCTCGCT 214
DB 340 TCGCAGACCCCTCAAGCCTGCGAAGTCAGCTCGCT 373

Search completed: June 15, 2003, 18:20:40
Job time : 43.9101 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 17:22:19 ; search time 93 6428 seconds
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Title: US-09-852-261-1

Perfect score: 517

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Searched: 1029858 seqs, 724030393 residues

Total number of hits satisfying chosen parameters: 2059716

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_NA:*

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- 2: /cgn2_6/ptodata/2/pubpna/PCR_NEW.seq:*
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- 11: /cgn2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
- 12: /cgn2_6/ptodata/2/pubpna/US10_PUBCOMB.seq:*
- 13: /cgn2_6/ptodata/2/pubpna/US60_NEW_PUB.seq:*
- 14: /cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	517	100.0	517	10	US-09-852-261-1
2	467.4	90.4	523	10	US-09-852-261-5
3	377.2	73.0	471	10	US-09-852-261-13
4	344.2	66.6	7260	9	US-10-136-639-4
5	344.2	66.6	7260	10	US-09-819-497-24
6	344.2	66.6	7260	10	US-09-880-107-3739
7	325.2	62.9	539	10	US-09-852-261-3
8	318.2	61.5	651	9	US-10-161-088-1
9	258.4	50.0	318	10	US-09-852-261-9
10	247.8	47.9	487	10	US-09-852-261-11
11	228	44.1	462	9	US-10-238-114-1
12	204.6	39.6	4532	10	US-09-930-377B-1
13	203.6	39.4	210	10	US-09-930-377B-2
14	202.8	39.2	390	9	US-10-179-046-13
15	202	39.1	286	9	US-10-161-088-3
16	140.2	27.1	213	9	US-10-076-816-9
17	140.2	27.1	213	9	US-10-077-381-9
18	123.8	23.9	621	9	US-10-280-826-40
19	123.8	23.9	621	10	US-09-921-398-40

20	108.6	21.0	480	9	US-10-280-826-38	Sequence 38, Appl
21	108.6	21.0	480	10	US-09-921-398-38	Sequence 38, Appl
22	75.4	14.6	411	10	US-09-960-352-2082	Sequence 2082, Ap
23	72.4	14.0	854	9	US-09-954-531-989	Sequence 989, App
24	71.8	13.9	237	9	US-10-136-841-3	Sequence 3, Appl
25	70.6	13.7	447	9	US-10-025-380-917	Sequence 917, App
26	70.6	13.7	447	10	US-09-922-217-917	Sequence 917, App
27	70.6	13.7	447	10	US-09-833-263-917	Sequence 917, App
28	70.4	13.6	437	9	US-10-066-543-663	Sequence 663, App
29	70.4	13.6	437	9	US-10-066-543-997	Sequence 997, App
30	70.4	13.6	518	9	US-10-066-543-1040	Sequence 1040, Ap
31	70.4	13.6	536	9	US-10-066-543-428	Sequence 428, App
32	70.4	13.6	543	9	US-10-136-841-1	Sequence 1, Appl
33	70.4	13.6	549	9	US-10-066-543-478	Sequence 478, App
34	70.4	13.6	574	9	US-10-025-380-918	Sequence 918, App
35	70.4	13.6	574	10	US-09-922-217-918	Sequence 918, App
36	70.4	13.6	574	10	US-09-833-263-918	Sequence 918, App
37	70.4	13.6	577	9	US-10-066-543-1137	Sequence 1137, App
38	70.4	13.6	579	9	US-10-066-543-1094	Sequence 1094, Ap
39	70.4	13.6	586	9	US-10-066-543-808	Sequence 808, App
40	70.4	13.6	1386	9	US-10-081-119-37	Sequence 144, App
41	70.4	13.6	1386	9	US-10-097-340-144	Sequence 293, App
42	70.4	13.6	1386	10	US-09-962-436-283	Sequence 294, App
43	70.4	13.6	1386	10	US-09-954-456-284	Sequence 294, App
44	70.4	13.6	1386	10	US-09-880-107-2092	Sequence 37, Appl
45	70.4	13.6	4350	9	US-10-125-181-37	Sequence 37, Appl

ALIGNMENTS

RESULT 1
US-09-852-261-1
US-09-852-261-1, Application US/09852261
Patient No. US2002008347781
GENERAL INFORMATION:
APPLICANT: GOLDSPINK, GEOFFREY
APPLICANT: TERENCE, GIORGIO
TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
FILE REFERENCE: 117-351
CURRENT APPLICATION NUMBER: US/09/852,261
CURRENT FILING DATE: 2001-05-10
PRIOR APPLICATION NUMBER: GB 0011278.9
PRIOR FILING DATE: 2000-05-10
NUMBER OF SEQ ID NOS: 14
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 517
TYPE: DNA
ORGANISM: Homo sapiens
US-09-852-261-1

Query Match 100.0%; Score 517; DB 10; Length 517;
Best Local Similarity 100.0%; Pred. No. 1.2e+159;
Matches 517; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	GGACCGGAGAGCGCTGCGGGGCTGAGTGGATGCTTCAGTTCGTGTGAGAC	60
DB	1	GGACCGGAGAGCGCTGCGGGGCTGAGTGGATGCTTCAGTTCGTGTGAGAC	60
QY	61	AGGGGGTTTTATTACACAGAGGATGATGCTCCAGAGTGGAGGCGGCTCAG	120
DB	61	AGGGGGTTTTATTACACAGAGGATGATGCTCCAGAGTGGAGGCGGCTCAG	120
QY	121	ACAGGATGCTGATGATGCTGCTCCAGAGTGGATGATGATGATGATGATGAT	180
DB	121	ACAGGATGCTGATGATGCTGCTCCAGAGTGGATGATGATGATGATGATGAT	180
QY	181	TGGCAGCCCTCAGAGCTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG	240
DB	181	TGGCAGCCCTCAGAGCTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG	240
QY	241	ATGCCCAAGAGCCGAGAGTATCAGCCCATCTACCAACAAGACGAGAGTCTAG	300

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DB 241 ATGCCAAGACCCAGAGATATACGCCCCCATCTACCAACAACAACAGAGCTCTAGAGA 300
QY 301 AGGAAAGAGATACATTTTGAAGAACACAGTAGAGGAGTGCAGGAACACAGACTACAG 360
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DB 361 GATGTAGAGACCCCTCTAGAGATGAAGAAAGACAGGCGCAGGACCCCTTGTGCT 420
QY 421 GCACAGTACCTGTAAACATTTGGAATACCGGCCAAAAAATAGTTGATCATTTCAAA 480
DB 421 GCACAGTACCTGTAAACATTTGGAATACCGGCCAAAAAATAGTTGATCATTTCAAA 480
QY 481 GATGCAATTTCCCAATGAATACAGAGTAACAT 517
DB 481 GATGCAATTTCCCAATGAATACAGAGTAACAT 517
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RESULT 2

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US-09-852-261-5
; Sequence 5, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPIRK, GEOFFREY
; APPLICANT: TERENCE, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 5
; LENGTH: 523
; TYPE: DNA
; ORGANISM: Oryctolagus cuniculus
US-09-852-261-5
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Query Match 90.4%; Score 467.4; DB 10; Length 523;
Best Local Similarity 96.2%; Pred. No. 2,5e-143;
Matches 501; Conservative 0; Mismatches 16; Indels 4; Gaps 2;

QY 1 GGAACCGAGAGAGCTGTGCGGGGCTGAGCTGTGTGATGCTCTTCACTTGTGTGAGAC 60
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QY 61 AGGGGCTTTATTTCAACAAGCCCAAGGATGAGCTCCAGCAAGTGGAGGGGCGCTCAG 120
DB 61 AGGGGCTTTATTTCAACAAGCCCAAGGATGAGCTCCAGCAAGTGGAGGGGCGCTCAG 120
QY 121 ACAAGCATCTGTGATGAGTGTCTCTCCGAGCTGTGATGAAGAGGCTGAGATGTAT 180
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QY 181 TGCGCACCCTCAAGCTGTGCGCAAGTCACTGCTCTGCTGCCAGGCGCCACAGCGAG 240
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QY 241 ATGCCCAAGACCCAGAGATATCAGCCCATCTACCAACAAGAAACAGAGTCTCA---G 297
DB 241 ATGCCCAAGACCCAGAGATATCAGCCCATCTACCAACAAGAAATGAAGTCTCAGAGG 300
QY 298 AGAAGGAAGAGATATTTGAAGAACACAAGTAGAGGAGTGCAGGAAACAAGACTA 357
DB 301 AGAAGGAAGAGATATTTGAAGAACACAAGTAGAGGAGTGCAGGAAACAAGACTA 360
QY 358 CAGGATGTA--GAAGACCTCTGTGAGAGTAGAAGAGACAGGCCACGCGAGACCTTTG 416
DB 361 CAGGATGTAAGAGACCTCTGTGAGAGTAGAAGAGACAGGCCACGCGAGACCTTTG 420
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QY 417 CTCTGACAGTACTGTAACATTTGAATACCGGCCAAAAAATAGTTGATCATT 476
DB 421 CTCTGACAGTACTGTAACATTTGAATACCGGCCAAAAAATAGTTGATCATT 480
QY 477 CAAGATGGCATTTCCCAATGAATACACAGTAACAT 517
DB 481 CAAGATGGCATTTCCCAATGAATACACAGTAACAT 521
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RESULT 3

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US-09-852-261-13
; Sequence 13, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPIRK, GEOFFREY
; APPLICANT: TERENCE, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; CURRENT FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 13
; LENGTH: 471
; TYPE: DNA
; ORGANISM: Oryctolagus cuniculus
US-09-852-261-13
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Query Match 73.0%; Score 377.2; DB 10; Length 471;
Best Local Similarity 87.8%; Pred. No. 1e-113;
Matches 455; Conservative 0; Mismatches 13; Indels 50; Gaps 2;

QY 1 GGAACCGAGAGAGCTGTGCGGGGCTGAGCTGTGTGATGCTCTTCACTTGTGTGAGAC 60
DB 1 GGAACCGAGAGAGCTGTGCGGGGCTGAGCTGTGTGATGCTCTTCACTTGTGTGAGAC 60
QY 61 AGGGGCTTTATTTCAACAAGCCCAAGGATGAGCTCCAGCAAGTGGAGGGGCGCTCAG 120
DB 61 AGGGGCTTTATTTCAACAAGCCCAAGGATGAGCTCCAGCAAGTGGAGGGGCGCTCAG 120
QY 121 ACAAGCATCTGTGATGAGTGTCTCTCCGAGCTGTGATGAAGAGGCTGAGATGTAT 180
DB 121 ACAAGCATCTGTGATGAGTGTCTCTCCGAGCTGTGATGAAGAGGCTGAGATGTAT 180
QY 181 TGCGCACCCTCAAGCTGTGCGCAAGTCACTGCTCTGCTGCCAGGCGCCACAGCGAG 240
DB 181 TGCGCACCCTCAAGCTGTGCGCAAGTCACTGCTCTGCTGCCAGGCGCCACAGCGAG 240
QY 241 ATGCCCAAGACCCAGAGATATCAGCCCATCTACCAACAAGAAACAGAGTCTCAGAGA 300
DB 241 ATGCCCAAGACTCAG----- 255
QY 301 AGAAGGAAGATACATTTGAAGAACACAAGTAGAGGAGTGCAGGAACACAGACTACAG 360
DB 256 ---AAGGAAGATACATTTGAAGAACACAAGTAGAGGAGTGCAGGAACACAGACTACAG 311
QY 361 GATGTA--GAAGACCTCTGTGAGAGTAGAAGAGACAGGCCACGCGAGACCTTTGCTC 419
DB 312 GATGTAAGAGACCTCTGTGAGAGTAGAAGAGACAGGCCACGCGAGACCTTTGCTC 371
QY 420 TGCAGAGTACTGTAAACATTTGAATACCGGCCAAAAAATAGTTGATCATTTCAA 479
DB 372 TGCAGAGTACTGTAAACATTTGAATACCGGCCAAAAAATAGTTGATCATTTCAA 431
QY 480 AGATGGCATTTCCCAATGAATACAGAGTAACAT 517
DB 432 AGATGGCATTTCCCAATGAATACAGAGTAACAT 469
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RESULT 4

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US-10-136-639-4
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Db 319 TGTGCCCCACTGSAACCTTACAAAGCACCCTTATTCCTGTCGCCACGCCACACTGAC 378
Qy 241 ATGCCCAAGACCAGAGATATCAGGCCCATCTTACCAACAAGACAGAGTCTCA---G 297
Db 379 ATGCCCAAGACATCAAGATCCCGCTTCTTATTCGACAAACAAGAAACAGACCTGAAAG 438
Qy 298 AGAAGGAAGAGAGATGATTTGAACAACAAGTGAAGAGAGTGAAGAGAGTGAAGAGAGTGA 357
Db 439 AGAAGGAAGAGAGATGATTTGAACAACAAGTGAAGAGAGTGAAGAGAGTGAAGAGAGTGA 498
Qy 358 CAGAGATGTA-GAAGACCCCTTCTGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 416
Db 459 CAGAGATGTAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 558
Qy 417 CTCTGACAGATTAAGTCTGTAAGATGTAAGTGAAGTGAAGTGAAGTGAAGTGAAGTGA 470
Db 559 CTGCTTGAGCAACCTGCAAAACATGAAACACCTTACCAATATATATATATATATATAT 618
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Db 619 ACATTTCAAGATGGGCAATTTCCCAATGAA 651
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RESULT 9

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US-09-852-261-9
; Sequence 9, Application US/09852261
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: TERENGI, GIORGIO
; APPLICANT: GOLDSPIK, GEOFFREY
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 9
; LENGTH: 318
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-852-261-9
```

```
Query Match 50.0%; Score 258.4; DB 10; Length 318;
Best Local Similarity 99.6%; Pred. No. 9, 5e-75;
Matches 259; Conservative 0; Mismatches 1; Indels 0; Gaps 0;
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Qy 1 GGACCGGAGAGCTCTGCGGGGCTGAGCTGTGATGCTCTTCACTGCTGTGTGAGAGAC 60
Db 1 GGACCGGAGAGCTCTGCGGGGCTGAGCTGTGATGCTCTTCACTGCTGTGTGAGAGAC 60
Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATATGCTCCAGAGAGTGGAGGCGGCTCAG 120
Db 61 AGGGGCTTTTATTTCAACAAGCCACAGGATATGCTCCAGAGAGTGGAGGCGGCTCAG 120
Qy 121 AAGGCAATCGTGAAGAGTGTCTTCCGAGAGCTGTATCTAAGAGAGCTGAGATGTAT 180
Db 121 AAGGCAATCGTGAAGAGTGTCTTCCGAGAGCTGTATCTAAGAGAGCTGAGATGTAT 180
Qy 181 TGCAGACCCCTCAAGCTGCGAGTCACTGCTGTGCTGCGGACCGCCACACCGCAG 240
Db 181 TGCAGACCCCTCAAGCTGCGAGTCACTGCTGTGCTGCGGACCGCCACACCGCAG 240
Qy 241 ATGCCCAAGACCCACAAGTA 260
Db 241 ATGCCCAAGACCCACAAGTA 260
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RESULT 10
US-09-852-261-11
; Sequence 11, Application US/09852261
```

```
; Patent No. US20020083477A1
; GENERAL INFORMATION:
; APPLICANT: GOLDSPIK, GEOFFREY
; APPLICANT: TERENGI, GIORGIO
; TITLE OF INVENTION: REPAIR OF NERVE DAMAGE
; FILE REFERENCE: 117-351
; CURRENT APPLICATION NUMBER: US/09/852,261
; PRIOR FILING DATE: 2001-05-10
; PRIOR APPLICATION NUMBER: GB 0011278.9
; NUMBER OF SEQ ID NOS: 14
; SOFTWARE: Patent Ver. 2.1
; SEQ ID NO 11
; LENGTH: 487
; TYPE: DNA
; ORGANISM: Rattus sp.
US-09-852-261-11
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Query Match 47.9%; Score 247.8; DB 10; Length 487;
Best Local Similarity 74.5%; Pred. No. 3, 6e-71;
Matches 391; Conservative 0; Mismatches 77; Indels 57; Gaps 4;
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Qy 1 GGACCGGAGAGCTCTGCGGGGCTGAGCTGTGATGCTCTTCACTGCTGTGTGAGAGAC 60
Db 1 GGACCGGAGAGCTCTTCCGGGGCTGAGCTGTGAGAGCTCTTCACTGCTGTGTGAGAGAC 60
Qy 61 AGGGGCTTTTATTTCAACAAGCCACAGGATATGCTCCAGAGAGTGGAGGCGGCTCAG 120
Db 61 AGGGGCTTTTACTTCAACAAGCCACAGTATATGCTCCAGAGTGGAGGCGGACCAAG 120
Qy 121 ACAAGCATCGTGAAGAGTGTCTTCCGAGAGCTGTATCTAAGAGAGCTGAGATGTAT 180
Db 121 ACGGGCATGTGTGATGATGCTTCTCCGAGAGCTGTATCTGAGAGAGCTGGAGATGTAC 180
Qy 181 TGCAGACCCCTCAAGCTGCGAGTCACTGCTGTGCTGCGGACCGCCACACCGCAG 240
Db 181 TGTGCTCCGCTGCAAGCTTCAAAAGTCAAGTCACTGCTTCCAGAGAGAGAGAGAG 240
Qy 241 ATGCCCAAGACCCACAAGTATCAAGCCCATCTACCAACAAGAGAGAGAGTCTCAGAGA 300
Db 241 ATGCCCAAGACTG----- 255
Qy 301 AGAAGAGAGTCACTTGAAGAACACAGATAGAGAGAGTGCAGAGAGAGAGAGACTACAG 360
Db 256 ---AAGGAAGTACTTGAAGAACACAGATAGAGAGAGAGAGAGAGAGAGAGAGAG 311
Qy 361 GATGTA-GAAGACCCCTTCTGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
Db 312 AATGTAGAGAGAGAGCTCCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 371
Qy 420 TGCACAGTACCTTAAACATTTGAATACCGGCA-----AAAATAACTTTGATCACA 473
Db 372 CTGAGAGACCTGCAAAACATCGGACACCTGCCAAATATCAATTAAGATCAATATCA 431
Qy 474 TTCAAGAT-GGCATTTTCCCAATGAATATACAGATTAAGAT 517
Db 432 TTTCAGATGTGGCATTTCCCTCATGATATACCAAGTAAACAT 476
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```
RESULT 11
US-10-238-114-1
; Sequence 1, Application US/10238114
; Publication No. US20030100073A1
; GENERAL INFORMATION:
; APPLICANT: Meriel
; APPLICANT: ANDREONI, Christine Michele
; TITLE OF INVENTION: IGF-1 AS FELINE VACCINE ADJUVANT, IN PARTICULAR AGAINST FELINE
; FILE REFERENCE: 454313-3165.1
; CURRENT APPLICATION NUMBER: US/10/238,114
; PRIOR FILING DATE: 2002-09-10
; PRIOR APPLICATION NUMBER: FR 01 11736
; PRIOR FILING DATE: 2001-09-11
; PRIOR APPLICATION NUMBER: US 60/318,666
```

PRIOR FILING DATE: 2001-09-12
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 462
TYPE: DNA
ORGANISM: Felis catus
US-10-238-114-1

Query Match 44.1%; Score 228; DB 9; Length 462;
Best Local Similarity 92.3%; Pred. No. 1,1e-64;
Matches 240; Conservative 0; Mismatches 20; Indels 0; Gaps 0;

QY 1 GGACCGGAGAGCGCTCTGCGGGGCTGAGCTGATGCTTCTAGTTCGTGTGAGAGC 60
DB 145 GGACCAAGAGAGCGCTCTGCGGGGCTGAGCTGATGCTTCTAGTTCGTGTGAGAGC 204
QY 61 AGGGGCTTTTATTTCAACAAGCCCAAGCGGTATGCTCCAGCAGTCGGAGCGCCTCAG 120
DB 205 AGGGGCTTTTATTTCAACAAGCCCAAGCGGTATGCTCCAGCAGTCGGAGCGCCTCAG 264
QY 121 ACAGGATCGTGATGATGCTGCTTCCGAGCTGTGATTAAGGAGGCTGAGATGAT 180
DB 265 ACAGGATCGTGATGATGCTGCTTCCGAGCTGTGATTAAGGAGGCTGAGATGAT 324
QY 181 TGGGACCCCTCAAGCCTGCGCAAGTCACTGCTCTGCTCCGCGCCAGCCACACCGAC 240
DB 325 TGTGACCCCTCAAGCCTGCGCAAGTCACTGCTCTGCTCCGCGCCAGCCACACCGAC 384
QY 241 ATGCCCAAGACCAAGAGTA 260
DB 385 ATGCCCAAGGCTCAGAAAGA 404

RESULT 12

US-09-930-377B-1

Sequence 1, Application US/09930377B
Patent No. US20020144296A1

GENERAL INFORMATION:
APPLICANT: Wheeler, Matthew B.
APPLICANT: Donovan, Sharon M.
APPLICANT: Bleck, Gregory T.
APPLICANT: Monaco-Seigel, Marcia
TITLE OF INVENTION: Animals Expressing Exogenous IGF-I in their Milk
FILE REFERENCE: 66-00
CURRENT APPLICATION NUMBER: US/09/930,377B
CURRENT FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: 60/225,474
PRIOR FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 4532
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: alpha-1A/IGF-I
US-09-930-377B-1

Query Match 39.6%; Score 204.6; DB 10; Length 4532;
Best Local Similarity 95.9%; Pred. No. 1,7e-56;
Matches 210; Conservative 0; Mismatches 9; Indels 0; Gaps 0;

QY 1 GGACCGGAGAGCGCTCTGCGGGGCTGAGCTGATGCTTCTAGTTCGTGTGAGAGC 60
DB 2046 GGACCGGAGAGCGCTCTGCGGGGCTGAGCTGATGCTTCTAGTTCGTGTGAGAGC 2105
QY 61 AGGGGCTTTTATTTCAACAAGCCCAAGCGGTATGCTCCAGCAGTCGGAGCGCCTCAG 120
DB 2106 AGGGGCTTTTATTTCAACAAGCCCAAGCGGTATGCTCCAGCAGTCGGAGCGCCTCAG 2165
QY 121 ACAGGATCGTGATGATGCTGCTTCCGAGCTGTGATTAAGGAGGCTGAGATGAT 180

DB 2166 ACAGGATCGTGATGATGCTGCTTCCGAGCTGTGATTAAGGAGGCTGAGATGAT 2225
QY 181 TGGGACCCCTCAAGCCTGCGCAAGTCACTGCTCTGCTC 219
DB 2226 TGGGACCCCTCAAGCCTGCGCAAGTCACTGATGATGCTC 2264

RESULT 13

US-09-930-377B-2

Sequence 2, Application US/09930377B
Patent No. US20020144296A1

GENERAL INFORMATION:
APPLICANT: Wheeler, Matthew B.
APPLICANT: Donovan, Sharon M.
APPLICANT: Bleck, Gregory T.
APPLICANT: Monaco-Seigel, Marcia
TITLE OF INVENTION: Animals Expressing Exogenous IGF-I in their Milk
FILE REFERENCE: 66-00
CURRENT APPLICATION NUMBER: US/09/930,377B
CURRENT FILING DATE: 2001-08-15
PRIOR APPLICATION NUMBER: 60/225,474
PRIOR FILING DATE: 2000-08-15
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 2
LENGTH: 210
TYPE: DNA
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: IGF-I
US-09-930-377B-2

Query Match 39.4%; Score 203.6; DB 10; Length 210;
Best Local Similarity 98.1%; Pred. No. 8e-57;
Matches 206; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 GGACCGGAGAGCGCTCTGCGGGGCTGAGCTGATGCTTCTAGTTCGTGTGAGAGC 60
DB 1 GGACCGGAGAGCGCTCTGCGGGGCTGAGCTGATGCTTCTAGTTCGTGTGAGAGC 60
QY 61 AGGGGCTTTTATTTCAACAAGCCCAAGCGGTATGCTCCAGCAGTCGGAGCGCCTCAG 120
DB 61 AGGGGCTTTTATTTCAACAAGCCCAAGCGGTATGCTCCAGCAGTCGGAGCGCCTCAG 120
QY 121 ACAGGATCGTGATGATGCTGCTTCCGAGCTGTGATTAAGGAGGCTGAGATGAT 180
DB 121 ACAGGATCGTGATGATGCTGCTTCCGAGCTGTGATTAAGGAGGCTGAGATGAT 180
QY 181 TGGGACCCCTCAAGCCTGCGCAAGTCACTGCTCTGCTC 210
DB 181 TGGGACCCCTCAAGCCTGCGCAAGTCACTGCTCTGCTC 210

RESULT 14

US-10-179-046-13

Sequence 13, Application US/10179046
Publication No. US20030013154A1

GENERAL INFORMATION:
APPLICANT: Crawford, Kenneth
Zator, Isabel
Innis, Michael
TITLE OF INVENTION: Pichia Secretary Leader for Protein Expression
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
ADDRESSSEE: Chiron Corporation
STREET: 4560 Horton Street
CITY: Emeryville
STATE: California
COUNTRY: United States
ZIP: 94608

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/179,046
FILING DATE: 25-Jun-2002
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/029,267
FILING DATE: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: Chung, Ling-Fong
REGISTRATION NUMBER: 36,482
REFERENCE/DOCKET NUMBER: 1165,100
TELECOMMUNICATION INFORMATION:
TELEPHONE: (510) 601-2704
TELEX: (510) 655-3542
INFORMATION FOR SEQ ID NO: 13:
SEQUENCE CHARACTERISTICS:
LENGTH: 390 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: other nucleic acid
DESCRIPTION: /desc = "Synthetic"
SEQUENCE DESCRIPTION: SEQ ID NO: 13:
US-10-179-046-13

Query Match 39.2%; Score 202.8; DB 9; Length 390;
Best Local Similarity 96.7%; Pred. NO. 2e-56; Indels 0; Gaps 0;
Matches 207; Conservative 0; Mismatches 7;

QY 1 GGACCGGAGACGCTGCGGGGCTGAGCTGATGATGCTTCAGTTCGATGATGAGAC 60
DB 160 GGACCGGAGACGCTGCGGGGCTGAGCTGATGATGCTTCAGTTCGATGATGAGAC 219
QY 61 AGGGGCTTTATTTACACAGCCCAAGGATGCTGCTCAGCAGCGGCGCTCAG 120
DB 220 AGGGGCTTTATTTACACAGCCCAAGGATGCTGCTCAGCAGCGGCGCTCAG 279
QY 121 ACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
DB 280 ACAGGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 339
QY 181 TCGGCAACCCCTCAGGCTGCCAAGTACGCTGCT 214
DB 340 TCGGCAACCCCTCAGGCTGCCAAGTACGCTGCT 373

RESULT 15

US-10-161-088-3
Sequence 3, Application US/10161088
Publication No. US2003007761A1
GENERAL INFORMATION:
APPLICANT: Parrow, Vendela
APPLICANT: Rosegren, Linda
TITLE OF INVENTION: NEW METHODS
FILE REFERENCE: 13425-111001
CURRENT APPLICATION NUMBER: US/10/161,088
CURRENT FILING DATE: 2002-05-31
PRIOR APPLICATION NUMBER: SE 0101934-8
NUMBER OF SEQ ID NOS: 3
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 3
LENGTH: 286
TYPE: DNA
ORGANISM: Homo sapiens
US-10-161-088-3

Query Match 39.1%; Score 202; DB 9; Length 286;
Best Local Similarity 88.0%; Pred. NO. 3.1e-56;

Matches 220; Conservative 0; Mismatches 30; Indels 0; Gaps 0;
QY 16 TCGGGGCTGAGCTGGTGGATGCTTCACATTTGTTGTGGAGACAGGGGCTTTATTTC 75
DB 18 TCGGGGCTGAGCTGGTGGATGCTTCACATTTGTTGTGGAGACAGGGGCTTTATTTC 77
QY 76 AACAGCCCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 135
DB 78 AACAGCCCAAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 137
QY 136 GAGTGTGCTTCCGAGCTGATCTAAGAGGCTGAGATGATGATGATGATGATGAT 195
DB 138 GAGTGTGCTTCCGAGCTGATCTAAGAGGCTGAGATGATGATGATGATGATGAT 197
QY 196 CCTGCCAAGTACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 255
DB 198 CTTCAAAAGCAGCCGCTCTATCGTGGCCAGCCACACTGACATGCCCAAGACTCAG 257
QY 256 AAGTATCAGC 265
DB 258 GCATGCAAGC 267

Search completed: June 15, 2003, 20:22:23
Job time : 95.6428 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: June 15, 2003, 15:41:03 ; Search time 1099.81 Seconds
(without alignments)
7613.181 Million cell updates/sec

Title: US-09-852-261-1

Perfect score: 517
Sequence: 1 gacacggagacgcctctgcg.....tgaatcaccaagtaaacat 517

Scoring table: IDENTITY_NUC
Gapop 10.0, Gapext 1.0

Searched: 16154066 seqs, 8097743376 residues

Total number of hits satisfying chosen parameters: 32308132

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :
EST:*
1: em_estbda:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_estl1:*
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27: em_gss_rod:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	331.6	64.1	558	9	A1503976 VM43608.x
C 2	330.6	63.9	673	14	BM984670 UI-CF-EC1
C 3	329.8	63.8	623	10	AW146128 AW146128
C 4	326.6	63.2	575	9	A1248089 qb56905.x
C 5	316.6	61.2	549	9	A1169253 EST215088
C 6	315.8	61.1	558	9	A1265629 uJ04607.x

C 7	314.8	60.9	498	9	AA542914
C 8	309	59.8	816	9	A1118218
C 9	303.6	58.7	594	12	BF383724
C 10	299.8	58.0	527	9	AA913900
C 11	289.6	56.0	642	9	A1876493
C 12	287.4	55.6	499	10	AA495481
C 13	276	53.4	468	9	A1169770
C 14	274.4	53.1	882	9	A1604642
C 15	268.2	51.5	430	9	A1478804
C 16	263.2	50.9	653	14	B0200567
C 17	258.4	50.0	608	9	AL599807
C 18	254.6	49.2	486	9	AA936559
C 19	254.2	49.2	521	10	AA493459
C 20	254.2	49.2	559	13	B1715603
C 21	254.2	49.2	621	13	B1211656
C 22	254	49.1	356	10	AA297586
C 23	253.2	49.0	595	9	A1573421
C 24	252.6	48.9	499	13	B1676839
C 25	252.6	48.9	500	9	AA945553
C 26	252.6	48.9	525	9	AA963258
C 27	251.4	48.6	482	9	AA456717
C 28	251.4	48.5	706	9	A1401719
C 29	249.4	48.2	525	9	A1598751
C 30	248.6	48.1	665	9	AA690767
C 31	247.8	47.9	559	13	B1715465
C 32	247.4	47.9	799	9	A1314558
C 33	247.2	47.8	499	13	B1294072
C 34	244.2	47.2	502	9	A1104659
C 35	243	47.0	561	13	B1714874
C 36	240.6	46.5	564	13	B1714981
C 37	237.4	45.9	588	13	B1715475
C 38	237.2	45.9	480	9	AA621551
C 39	236.8	45.8	512	9	A1876203
C 40	233.8	45.0	637	10	AA413016
C 41	233.6	45.0	779	9	AA867155
C 42	231	44.7	473	9	AA451360
C 43	230.8	44.6	773	13	B1445500
C 44	230.2	44.5	475	9	A1033043
C 45	227.6	44.0	474	9	A1526955

ALIGNMENTS

RESULT 1
A1503976/c 558 bp mRNA linear EST 11-MAR-1999
LOCUS
DEFINITION
vm43608.x1 Stratiogene mouse diaphragm (#937303) Mus musculus CDNA
clone IMAGE:1001007 3' similar to gb:X04482 Mouse mRNA for
preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.

ACCESSION
A1503976
VERSION
A1503976.1 GI:4401827
KEYWORDS
SOURCE
ORGANISM
Mus musculus
house mouse.
EST.

REFERENCE
AUTHORS
Marrin,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,Y., Person
B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schurr,R., Ritter
E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
Waterston,R. and Wilson,R.
The WashU-NCI Mouse EST Project 1999
Unpublished (1999)
CONTACT: Marrin M/WashU-NCI Mouse EST Project 1999
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: mouseest@wustl.wustl.edu
This clone is available royalty-free through LNL; contact the
IMAGE Consortium (info@image.lln.gov) for further information.

TITLE
JOURNAL
COMMENT

QY 241 ATGCCAAGAGCCCAAGATATCAGGCCCTCTTACCAACAGAACAGCAAGTCTCAGGA 300
 |||||||
 Db 233 ATGCCAAGAGCCCAAG----- 239
 QY 301 AGGAAGAAGAGTACATTTGAAAGAACAGAGAGAGGAGTGCAGGAACAGAACTACAG 360
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 Db 238 ----AAGAGAGTACATTTGAAAGAACAGAGTGAAGAGAGTGCAGGAACAGAACTACAG 183
 QY 361 GATGTA-GAAGACCTTCTGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 419
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 Db 182 GATGTAAG 123
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 QY 420 TGCAC-AGTTACCTG-TAAACATTCGAATACCGGAGAGAGAGAGAGAGAGAGAGAG 477
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 Db 122 TGCAGAGTACCTGTTAACTTTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 63
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 QY 478 AAGAT-GGCATTTCCCAATGAAATACAGATTAACAT 517
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 Db 62 AAGATGGGCGTTTCCCAATGAAATACAGATTAACAT 22
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RESULT 3
 AM146128/c 523 bp mRNA linear EST 10-OCT-2000
 LOCUS um37e10.x1 Sugano mouse embryo mewa Mus musculus cDNA clone
 DEFINITION IMAGE:2247498.3' similar to gb:X04482 Mouse mRNA for
 preproinsulin-like growth factor IB (MOUSE);, mRNA sequence.
 AM146128
 ACCESSION AM146128.1 GI:6167864
 VERSION
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.

REFERENCE 1 (bases 1 to 523)
 AUTHORS Maira,M., Hillier,L., Kucaba,T., Martin,J., Beck,C., Wylie,T.,
 Underwood,K., Steptoe,M., Theising,B., Allen,M., Bowers,T., Person
 B., Swaller,T., Gibbons,M., Pape,D., Harvey,N., Schuck,R., Rittler
 E., Kahn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R.,
 Waterson,R. and Wilson,R.
 The WashU-NCI Mouse EST Project 1999
 Unpublished (1999)
 TITLE Contact: Maira M/WashU-NCI Mouse EST Project 1999
 JOURNAL Washington University School of Medicine
 COMMENT 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MG1:1006958
 Seq primer: custom primer used
 High quality sequence stop: 499.

FEATURES

Source
 1..623
 Location/Qualifiers
 /organism="Mus musculus"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:2247498"
 /clone_lib="Sugano mouse embryo mewa"
 /dev_stage="embryo, 14 dpc"
 /lab_host="DH10B"
 /note="Vector: pME18S-FL3; Site 1: DraIII (CACTGATG);
 Site 2: DraIII (CAACCATG); 1st strand cDNA was primed
 with an oligo(dT) primer [ATGTGGCTTTTCTTTTCTTTT];
 double-stranded cDNA was ligated to a DraIII adaptor
 [GTGGCTTCTG], digested and cloned into pGEMT vector (5' site
 CACTGATG, 3' site CACCATG). XhoI should be used to isolate the cDNA
 insert. Size selection was performed to exclude fragments
 <1.5kb. Library constructed by Dr. Sumio Sugano
 (University of Tokyo Institute of Medical Science).

Custom primers for sequencing: 5' end primer
 CTTCGCTTAAAGCTGG and 3' end primer
 CGACCTGCACCTGCAGCA.
 BASE COUNT 123 a 138 c 170 g 191 t 1 others

Query Match 63.8%; Score 329.8; DB 10; Length 623;
 Best Local Similarity 80.6%; Pred. No. 5e-87;
 Matches 425; Conservative 0; Mismatches 92; Indels 10; Gaps 3;

QY 1 GGACCGAGAGCGCTCTCGGGGCTGAGCTGTGATCTTTAGTTCTGTGTGAGAC 60
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 Db 541 GGACCGAGAGCGCTCTTCGGGGCTGAGCTGTGATCTTTAGTTCTGTGTGAGAC 482
 |||||||
 QY 61 AGGGGCTTTATTTCACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 120
 |||||||
 Db 481 AGGGGCTTTATTTCACCAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 422
 |||||||
 QY 121 ACAGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 180
 |||||||
 Db 421 ACAGCATCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 362
 |||||||
 QY 181 TGGGCAACCCCTCAGAGCTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 240
 |||||||
 Db 361 TGGGCAACCCCTCAGAGCTGCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCAAGTCA 302
 |||||||
 QY 241 ATGCCAAG 297
 |||||||
 Db 301 ATGCCAAG 242
 |||||||
 QY 298 AGAAG 357
 |||||||
 Db 241 AGAAG 182
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 QY 358 CAGAGATGA-GAAGACCTCTGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 416
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 Db 181 CAGAGATGAAG 122
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 QY 417 CTCTGCACAGTCTTAACTTGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 470
 |||||||
 Db 121 CTCTGCACAGTCTTAACTTGAAGATGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 62
 |||||||
 QY 471 ACATTTCAAGATGAG 517
 |||||||
 Db 61 ACATTTCAAGATGAG 15
 |||||||

RESULT 4
 A1248089/c 575 bp mRNA linear EST 01-DEC-1998
 LOCUS qh69f05.x1 Soares fetal_liver_spleen_INFIS_S1 Homo sapiens cDNA
 DEFINITION qh69f05.1849953.3' similar to gb:X57025_rnal INSULIN-LIKE
 GROWTH FACTOR 1A PRECURSOR (HOMAN);, mRNA sequence.
 A1248089
 ACCESSION A1248089.1 GI:3843486
 VERSION
 KEYWORDS
 SOURCE human.
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE 1 (bases 1 to 575)
 AUTHORS NCI-CCAP http://www.ncbi.nlm.nih.gov/ncicap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.

FEATURES
 Email: cga@remail.nih.gov
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 Insert Length: 918 Std Error: 0.00
 Seq primer: -40UP from Glibco
 High quality sequence stop: 380.
 Location/Qualifiers

source

1. 575
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone="IMAGE:194953"
/clone_lib="Scares_fetal_liver_spleen_infls_si"
/sex="male"
/dev stage="20 week-post conception fetus"
/lab host="DH10B (ampicillin resistant)"
/note="Organ: Liver and Spleen; Vector: pT73D (Pharmacia) with a modified polylinker; Site_1: Pac I; Site_2: Eco RI; This is a subtracted version of the original Soares fetal liver spleen INFLS library. 1st strand cDNA was primed with a Pac I - Oligo(dT) primer [5', AACTGAGATTATTAAGATCTTTTCTTTTCTTTT 3'], double-stranded cDNA was ligated to Eco RI adaptors (Pharmacia), digested with Pac I and cloned into the Pac I and Eco RI sites of the modified pT73 vector. Library went through one round of normalization. Library constructed by Bento Soares and M.Fatima Bonaldo."

BASE COUNT 135 a 152 c 131 g 156 t 1 others

Query Match 63.2%; Score 326.6; DB 9; Length 575;
Best Local Similarity 86.6%; Pred.No.4.4e-86;
Matches 438; Conservative 0; Mismatches 15; Indels 53; Gaps 5;

Db 16 TGGGGGCTGAGCTGTGTGATGCTCTTCACTTGTGTGTGAGACAGGGGCTTTATTTC 75
551 TGGGGGCTGAGCTGTGTGATGCTCTTCACTTGTGTGTGAGACAGGGGCTTTATTTC 492

QY 76 AACAGAGCCACAGGATGTGCTCCAGAGTCGAGAGGGGCGCTCAGACAGGATCGTGAT 135
491 AACAGAGCCACAGGATGTGCTCCAGAGTCGAGAGGGGCGCTCAGACAGGATCGTGAT 432

Db 136 GAGTGTCTTCGCGAGAGCTGTATCTAAGAGAGCTGAGATGTATTGCGGACCCCTCAAG 195
431 GAGTGTCTTCGCGAGAGCTGTATCTAAGAGAGCTGAGATGTATTGCGGACCCCTCAAG 372

QY 196 CCTCCAGAGTACGCTGCTCTGTCTGCGGAGCGGACGACGACATGCCAAGACCCAG 255
371 CCTCCAGAGTACGCTGCTCTGTCTGCGGAGCGGACGACGACATGCCAAGACCCAG 312

Db 256 AAGTATAGCCCCCATCTACCAACAGAACAGAAAGTCTCAGAGAAAGAGAAATAC 315
311 -----AAGAAATGACA 301

QY 316 TTTAAGACACAACTGTAGAGGAGTGCAGAAACAGAACTACAGATGTA-GAAGACC 374
300 TTTAAGACACAACTGTAGAGGAGTGCAGAAACAGAACTACAGATGTAAGAGACC 241

Db 375 TTTCGAGAGTGAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 433
240 TTTCGAGAGTGAAGAGAGTGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 181

QY 434 -TAAACATTTGAATATCGCGCCAAAAAATTAAGTTGATACATTTCAAGAT-GGCATTT 491
180 TTAACATTTGAATATCGCGCCAAAAAATTAAGTTGATACATTTAAAGATGAGCGTTTC 121

Db 492 CCCCATGAATATACAGAAATTAACAT 517
120 CCCCATGAATATACAGAAATTAACAT 95

RESULT 5
A1169253 549 bp mRNA linear EST 08-JAN-1999
LOCUS E87215088 Normalized rat kidney, Bento Soares Rattus sp. cDNA clone
DEFINITION R1169253 end, mRNA sequence.
ACCESSION A1169253
VERSION A1169253.1 GI:4134375
KEYWORDS EST.
SOURCE Rattus sp.
ORGANISM Rattus sp.

REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT

1 (bases 1 to 549)
Lee,N.H., Glodex,A., Chandra,I., Mason,T.M., Quackenbush,J.,
Kerlavage,A.R. and Adams,M.D.
Rat Genome Project: Generation of a Rat EST (EST) Catalog & Rat
Gene Index
Unpublished (1998)
On Oct 6, 1998 this sequence version replaced gi:3705561.
Other ESTs: TC50779
Contact: Lee, NH
The Institute for Genomic Research
9712, Medical Center Drive, Rockville, MD 20850, USA
Tel: (301)-838-3529
Fax: (301)-838-0208
Email: nhlee@igf.org
Seq primer: M13-21.

FEATURES
source
Location/Qualifiers
1..549
/organism="Rattus sp."
/db_xref="taxon:10118"
/clone="R116923"
/note="Organ: Kidney; Vector: pT73pac; Site_1: EcoRI;
Site_2: NotI"

BASE COUNT 112 a 140 c 133 g 164 t

Query Match 61.2%; Score 316.6; DB 9; Length 549;
Best Local Similarity 80.8%; Pred.No.4e-83;
Matches 421; Conservative 0; Mismatches 89; Indels 11; Gaps 4;

Db 8 AGACGCTCGCGGCTGAGTGTGATGCTCTTCACTTGTGTGTGAGACAGGGGCT 67
549 AGACGCTCGCGGCTGAGTGTGATGCTCTTCACTTGTGTGTGAGACAGGGGCT 490

QY 68 TTTATTTCACAGCCACAGGATGTGCTCAGAGAGCGAGAGGGCGCTCAGACAGGCA 127
489 TTTATTTCACAGCCACAGGATGTGCTCAGAGAGCGAGAGGGCGCTCAGACAGGCA 430

Db 128 TCGTGATGAGTGTGCTTCGAGAGCTGTATCTAAGAGAGCTGAGATGTATTGCGAC 187
429 TCGTGATGAGTGTGCTTCGAGAGCTGTATCTAAGAGAGCTGAGATGTATTGCGAC 370

QY 188 CCTCAAGCTGCCAGAGTACGCTGCTGTCCGCGGAGGCGGACGACGACGACATGGCCA 247
369 CCTCAAGCTGCCAGAGTACGCTGCTGTCCGCGGAGGCGGACGACGACATGGCCA 310

Db 248 AGACCCAGAGTATAGGCCGCCCATCTACCAACAGAACAGAAAGTCTCA---GAGAAGA 304
309 AGACCCAGAGTATAGGCCGCCCATCTACCAACAGAACAGAAAGTCTCAAGAGAAGA 250

QY 305 AAGGAATGATTTGAGACACAACTAGAGGAGTGCAGAAACAAACTACAGAGTG 364
249 AAGGAATGATTTGAGACACAACTAGAGGAGTGCAGAAACAAACTACAGAGTG 190

Db 365 TA-GAAGACCTTCGAGAGTGAAGAGAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 423
189 TAGAGAGAGCTCCCGAGAGAACAGAAATGCGAGCTACCGGAAATCTTTCGCGCTG 130

QY 424 CAGTTACTGTAAACATTGGAATGCCGCCA-----AAAATTAAGTTGATACATTT 477
129 AGCAACCTGCAAAACATCGAAGACCTGCGCAATATCATATATGATTCAATACATTTTC 70

Db 478 AAGAT-GGCATTTCCCAATGAATATACAGAGTAACAT 517
69 AAGATGGGCATTTCCCTCAATGAATATACAGAGTAACAT 29

RESULT 6
A1265629 558 bp mRNA linear EST 18-NOV-1998
LOCUS A1265629/c

DEFINITION	u1040707.x1.Sugano mouse liver m1a.Mus musculus cDNA clone IMAGe:1890901.3', similar to gb:U04482 Mouse mRNA for preproinsulin-like growth factor IB (MOUSE), mRNA sequence.
ACCESSION	A1265629
VERSION	A1265629.1 GI:3883787
KEYWORDS	EST.
SOURCE	house mouse.
ORGANISM	Mus musculus
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 558)
AUTHORS	Maria,M., Hillier,L., Allen,M., Bowles,M., Dietrich,N., Dubuque,T., Geisel,S., Kucaba,T., Lacy,M., Le,M., Martin,J., Morris,M., Schellenberg,K., Steptoe,M., Tan,F., Underwood,K., Moore,B., Theising,B., Wylie,T., Lennon,G., Soares,B., Wilson,R. and Waterston,R.
TITLE	The WashU-HMI Mouse EST Project
JOURNAL	Unpublished (1996)
COMMENT	Contact: Maria M/Mouse EST Project WashU-HMI Mouse EST Project Washington University School of Medicine 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108 Tel: 314 286 1800 Fax: 314 286 1810 Email: mouseest@wustl.edu This clone is available royalty-free through LNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. M1:975325
FEATURES	Seq primer: custom primer used High quality sequence stop: 445.
SOURCE	Location/Qualifiers 1..558 /organism="Mus musculus" /strain="C57BL" /db_xref="taxon:10090" /clone="IMAGE:1890901" /clone_1ib="Sugano mouse liver m1a" /sex="female" /dev_stage="adult" /lab_host="DH10B" /note="Organ: liver; Vector: pME185-FL3; Site:1: DraIII (CACCATGG); Site:2: DraIII (CACCATGG); 1st strand cDNA was primed with an oligo(dT) primer [ATGGGCGCTTTTCTTTTCTTTT]; double-stranded cDNA was ligated to a DraIII adaptor [TGTGGCGCTTACTGG], digested and cloned into distinct DraIII sites of the pME185-FL3 vector (5' site CACCATGG, 3' site CACCATGG). XhoI should be used to isolate the cDNA insert. Size selection was performed to exclude fragments <1.5kb. Library constructed by Dr. Sumio Sugano (University of Tokyo Institute of Medical Science). Custom primers for sequencing: 5' end primer CTTGCTCTTAAAGCTGG and 3' end primer CACCTGGAGCTGAGACA."
BASE COUNT	106 a 135 c 156 g 161 t
ORIGIN	
Query Match	61.1%; Score 315.8; DB 9; Length 558;
Best Local Similarity	80.8%; Pred No. 7e-83;
Matches 408; Conservative 0;	Mismatches 87; Indels 10; Gaps 3
0Y	1 GGACGGAGAGAGCGCTGCGGGCGGTGAGCTGGTGGATGCTCTTCAGTTGCTGTGGAGAC 60
Db	
506	GGACGAGAGACCCCTTGGCGGGCTAGCTGGTGGATGCTCTTCAGTTGCTGTGGAGAC 447
0Y	61 AGGGCGTTTATTTCAACAGCCACAGGCTATAGCTCTCACAACTGGAGGGCGCTCAG 120
Db	
446	AGGGCGTTTACTTCAACAGCCACAGGCTATAGCTCTCACAACTGGAGGGCGCTCAG 387
0Y	121 ACAGGATCGTGGATAGTGTGCTTCCGGAAGCTTGATCTAAGAGAGCTGGAATGTAT 180
Db	
386	ACAGGATGTGATGATGATGTGCTTCCGGAAGCTTGATCTAAGAGAGCTGGAATGTAT 327
0Y	181 TGGCACCCTCAAGCTCCCAAGTACAGTGCCTGTTCGCTGCCACAGCGCACACCGAC 240

Db	Accession	Version	Source	Organism	Reference	Authors	Title	Journal	Comment
Db	326	1	ACATTTGAGCAGCCTTTCCTTCCGTTGCGCCAGCGCCACTGAC	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	241	1	ATGCCCCAAGACCAGAGATATCAGCCCCCATCTTACCAACAGAACAGAGTCTCA--G	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	266	1	ATGCCCAAGACTCAGAGAGTCCCTCCCTCTATCGCAACAGAAAGAGCTGCAAGG	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	298	1	AGAGGAAAGAGAACTACATTTTGAAGACACACAGTAGAGGGGAGTGCAGAAACAGAACTA	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	206	1	AGAGGAAAGAGAACTACATTTTGAAGACACACAGTAGAGGGGAGTGCAGAAACAGAACTA	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	358	1	CAGAGATGTA-GAAGACCCCTTCTGAGAGTGAAGAGACAGCCAGCCAGACCTTTG	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	146	1	CAGATATGAGAGAGAGAGCTCCACGAGAGAGAAATGCAATATGCAATATGCAATATG	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	417	1	CTCTGACAGCTTACCTGTAAACATTTGAGTACCGGCA-----AAAATAGTTTATC	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	86	1	CTGCTTGAGCAGCACTGCAAAACAGAAACACGTCACCAATATACATATATATGTCATA	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	471	1	ACATTTGAGCAGCCTTTCCTTCCGTTGCGCCAGCGCCACTGAC	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	26	1	ACATTTGAGCAGCCTTTCCTTCCGTTGCGCCAGCGCCACTGAC	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	326	1	ATGCCCCAAGACCAGAGATATCAGCCCCCATCTTACCAACAGAACAGAGTCTCA--G	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	241	1	ATGCCCCAAGACCAGAGATATCAGCCCCCATCTTACCAACAGAACAGAGTCTCA--G	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	266	1	ATGCCCAAGACTCAGAGAGTCCCTCCCTCTATCGCAACAGAAAGAGCTGCAAGG	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	298	1	AGAGGAAAGAGAACTACATTTTGAAGACACACAGTAGAGGGGAGTGCAGAAACAGAACTA	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	206	1	AGAGGAAAGAGAACTACATTTTGAAGACACACAGTAGAGGGGAGTGCAGAAACAGAACTA	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	358	1	CAGAGATGTA-GAAGACCCCTTCTGAGAGTGAAGAGACAGCCAGCCAGACCTTTG	Human	EST 19-AUG-1997	1997	1997	1997	1997
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Db	417	1	CTCTGACAGCTTACCTGTAAACATTTGAGTACCGGCA-----AAAATAGTTTATC	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	86	1	CTGCTTGAGCAGCACTGCAAAACAGAAACACGTCACCAATATACATATATATGTCATA	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	471	1	ACATTTGAGCAGCCTTTCCTTCCGTTGCGCCAGCGCCACTGAC	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	26	1	ACATTTGAGCAGCCTTTCCTTCCGTTGCGCCAGCGCCACTGAC	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	326	1	ATGCCCCAAGACCAGAGATATCAGCCCCCATCTTACCAACAGAACAGAGTCTCA--G	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	241	1	ATGCCCCAAGACCAGAGATATCAGCCCCCATCTTACCAACAGAACAGAGTCTCA--G	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	266	1	ATGCCCAAGACTCAGAGAGTCCCTCCCTCTATCGCAACAGAAAGAGCTGCAAGG	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	298	1	AGAGGAAAGAGAACTACATTTTGAAGACACACAGTAGAGGGGAGTGCAGAAACAGAACTA	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	206	1	AGAGGAAAGAGAACTACATTTTGAAGACACACAGTAGAGGGGAGTGCAGAAACAGAACTA	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	358	1	CAGAGATGTA-GAAGACCCCTTCTGAGAGTGAAGAGACAGCCAGCCAGACCTTTG	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	146	1	CAGATATGAGAGAGAGAGCTCCACGAGAGAGAAATGCAATATGCAATATGCAATATG	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	417	1	CTCTGACAGCTTACCTGTAAACATTTGAGTACCGGCA-----AAAATAGTTTATC	Human	EST 19-AUG-1997	1997	1997	1997	1997
Db	86	1	CTGCTTGAGCAGCACTGCAAAACAGAAACACGTCACCAATATACATATATATGTCATA	Human	EST 19-AUG-1997	1997	1997	1997	1997

ORIGIN

Query Match 60.9%; Score 314.8; DB 9; Length 498;
 Best Local Similarity 86.2%; Pred. No. 1.3e-82;
 Matches 450; Conservative 0; Mismatches 17; Indels 55; Gaps 7;

Y 1 GGACCCGAGACGCTGCGGGGCGG-TGAGCTGGTGGATGCTCTTCAATTGCTGTGGAGA 59
 D 476 GGACCCGAGACGCTGCGGGGCGG-TGAGCTGGTGGATGCTCTTCAATTGCTGTGGAGA 417
 Y 60 CAGGGGCTTTATTTACAGACCCACAGAGGATGCTCCAGAGCTGCGAGGCGGCTCA 119
 D 416 CAGGGGCTTTATTTACAGACCCACAGAGGATGCTCCAGAGCTGCGAGGCGGCTCA 358
 Y 120 GAGAGGATGCTGGATGAGTGGTCTTCCGAGAGCTGATCTAAGAGAGCTGGAATGTA 179
 D 357 GACAGGATGCTGGATGAGTGGTCTTCCGAGAGCTGATCTAAGAGAGCTGGAATGTA 298
 Y 180 TTGCGACACCCCTGACAGCTGCGAGTCACTGCTGCTGCGGACGCGCACACCA 239
 D 297 TTGCGACACCCCTGACAGCTGCGAGTCACTGCTGCTGCGGACGCGCACACCA 238
 Y 240 CATGCCAGACCCAGAGATGATCAGCCCATCTACACAGACAGCAAGTCTAGAG 299
 D 237 CATGCCAGACCCAGAGATGATCAGCCCATCTACACAGACAGCAAGTCTAGAG 222
 Y 300 AAGGAAAGAGATGATGATGAGACAGAGTAGAGGAGTGCAGAGAAACAGACTACA 359
 D 221 -----AAGGAAAGATGATGATGAGACAGAGTAGAGGAGTGCAGAGAAACAGACTACA 167
 Y 360 GATGTA-GAAGACCTTCTGAGAGAGTGAAGAGACAGGCGCCAGAGACCTTTGCT 418
 D 166 GATGTA-GAAGACCTTCTGAGAGAGTGAAGAGACAGGCGCCAGAGACCTTTGCT 107
 Y 419 CTGAC-AGTACTCTG-TAAGCATGGAATCCGCAAAATAGTTGATCACTAT 476
 D 106 CTGACAGAGTACTCTG-TAAGCATGGAATCCGCAAAATAGTTGATCACTAT 47
 Y 477 CAAGAT-GGCAATTTCCCAATGAATACACAGATAAAT 517
 D 46 AAAAGATGGGCTTTCCCAATGAATACACAGATAAAT 5
 RESULT 8 816 bp mRNA linear EST 02-SEP-1998
 A119218
 LOCUS
 DEFINITION u94h02.y1 Sugano mouse embryo mewa Mus musculus cDNA clone
 IMAGE:1498803 5' similar to gb:X0482 Mouse mRNA for
 preproinsulin-like growth factor IB (MUSEF);, mRNA sequence.
 A119218
 ACCESSION A119218.1 GI:3519542
 VERSION
 KEYWORDS
 SOURCE house mouse.
 ORGANISM Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 816)
 REFERENCE
 AUTHORS Marra, M., Hillier, L., Allen, M., Bowles, M., Dietrich, N., Dubuque, T.,
 Gettel, S., Kucada, T., Lacy, M., Le, M., Martin, J., Morris, M.,
 Schellensberg, K., Steptoe, M., Tan, F., Underwood, K., Moore, B.,
 Theising, B., Wylie, T., Lennon, G., Soares, B., Wilson, R. and
 Waterston, R.
 TITLE The WashU-HMI Mouse EST Project
 JOURNAL Unpublished (1996)
 COMMENT Contact: Marra M/Mouse EST Project
 WashU-HMI Mouse EST Project
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LIND; contact the
 IMAGE Consortium (info@image.lind.gov) for further information.

MG1:936407
 Seq primer: custom primer used
 High quality sequence stop: 473.
 Location/Qualifiers
 1. 816
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 /strain="C57BL/6"
 /db_xref="taxon:10090"
 /clone="IMAGE:1498803"
 /clone_11b="Sugano mouse embryo mewa"
 /dev_stage="embryo, 14 dpc"
 /lab_host="DH10B"
 /note="Vector: pME18S-FL3; Site 1: DraII (CACTGTG);
 Site 2: DraII (CAGCATG); 1st strand cDNA was primed
 with an oligo(dT) primer (ATGGGCGCTTTTCTTTTCTTTT);
 double-stranded cDNA was ligated to a DraII adaptor
 (TGTGGCTCTG), digested and cloned into distinct DraII
 sites of the pME18S-FL3 vector (5' site CACTGTG, 3' site
 CAGCATG). XhoI should be used to isolate the cDNA
 insert. Size selection was performed to exclude fragments
 <1.5kb. Library constructed by Dr. Sumio Sugano
 (University of Tokyo Institute of Medical Science).
 Custom primers for sequencing: 5' end primer
 CTTCGCTTAAGCTGCG and 3' end primer
 CGACCTGAGCTCGAGCA." 230 a 219 c 172 g 187 t 8 others

BASE COUNT 230 a 219 c 172 g 187 t 8 others

Query Match 59.8%; Score 309; DB 9; Length 816;
 Best Local Similarity 80.2%; Pred. No. 8.2e-81;
 Matches 384; Conservative 0; Mismatches 91; Indels 4; Gaps 2;

Y 1 GGACCGAGACGCTGCGGGGCTGAGCTGTGATGCTCTTCAATTGCTGTGGAGC 60
 D 323 GGACCGAGACGCTTTCGGGGCTGAGCTGTGATGCTCTTCAATTGCTGTGGAGC 382
 Y 61 AGGGCTTTTATTTAAAGAGCCACAGGATGCTCCAGAGCGGCGCTCAG 120
 D 383 AGGGCTTTTATTTAAAGAGCCACAGGATGCTCCAGAGCGGCGCTCAG 442
 Y 121 ACAGCATGTGATGATGATGCTGCTTCGAGAGCTGTGATGAGAGAGCTGAT 180
 D 443 ACAGCATGTGATGATGATGCTGCTTCGAGAGCTGTGATGAGAGAGCTGAT 502
 Y 181 TGCGACCCCTTAACCTTCCCAAGTACGCTGTGCTGCCAGCCACACCGAC 240
 D 503 TGCGACCCCTTAACCTTCCCAAGTACGCTGTGCTGCCAGCCACACCGAC 562
 Y 241 ATGCCCAAGCCAGAGATGAGCCCATCTACCAAGAGACAGAGCTCTCA--G 297
 D 563 ATGCCCAAGCCAGAGATGAGCCCATCTACCAAGAGAGAGAGCTCTCA--G 622
 Y 298 AGAAGAAAGAGATGATTTGAGACACAGATGAGAGGAGTGCAGAGAAACAGACTA 357
 D 623 AGAAGAAAGAGATGATTTGAGACACAGATGAGAGGAGTGCAGAGAAACAGACTA 682
 Y 358 CAGGATGTA-GAAGACCTTCTGAGAGTGAAGAGAGAGAGCCAGAGACCTTTG 416
 D 683 CAGGATGTA-GAAGACCTTCTGAGAGTGAAGAGAGAGAGAGAGAGAGAGAGCTTTG 742
 Y 417 CTCTGACAGTACTGTAACATTTGAAATACCGCCCAAAATATAGTTGATCACT 475
 D 743 CTCTGACAGTACTGTAACATTTGAAATACCGCCCAAAATATAGTTGATCACT 801
 RESULT 9 594 bp mRNA linear EST 27-NOV-2000
 BF383724
 LOCUS
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 mRNA sequence.
 A119218
 ACCESSION BF383724.1 GI:11365029
 VERSION
 KEYWORDS EST.

SOURCE house mouse.
ORGANISM Mus musculus
REFERENCE Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 594)
AUTHORS NIH-MGC <http://mgi.nci.nih.gov/>.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
Tissue Procurement: Jeffrey E. Green, M.D.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LMNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LMNL at: <http://image.llnl.gov>
Plate: LLM9527 row: p column: 08
High quality sequence stop: 589.
Location/Qualifiers
1..594
/organism="Mus musculus"
/strain="FVB/N"
/db_xref="taxon:10090"
/clone_image="4194295"
/clone_lib="NCI-CGAP_L19"
/lab_host="DH10B (T1 phage-resistant)"
/note="Organ: liver; Vector: pCMV-Sport6; Site: 1; NotI; Site: 2; SalI; Cloned unidirectionally. Primer: oligo dt. Average insert size 1.9 kb. Constructed by Life Technologies. Note: this is a NCI-CGAP library."
BASE COUNT 175 a 162 c 142 g 115 t
ORIGIN
Query Match 58.7%; Score 303.6; DB 12; Length 594;
Best Local Similarity 80.7%; Pred. No. 3e-79; Mismatches 84; Indels 10; Gaps 3;
Matches 394; Conservative 0;

16 TCGGGGGCTGAGCTGGATGCTCTTCAGTTCGTGTGAGACAGGGGCTTTATTTTC 75
107 TCGGGGGCTGAGCTGGATGCTCTTCAGTTCGTGTGAGACAGGGGCTTTATTTTC 166
76 AACAGCCACAGGGTATGCTCCAGCAGCTGGAGGGGCTCCAGAGGATCGTGAT 135
167 AACAGCCACAGGGTATGCTCCAGCAGCTGGAGGGGCTCCAGAGGATCGTGAT 226
136 GAGTCTGCTTCGAGCTGTGATCTAAGAGAGGCTGAGATGTATTGCCACCCCTCAAG 195
227 GAGTCTGCTTCGAGCTGTGATCTAAGAGAGGCTGAGATGTATTGCCACCCCTCAAG 286
196 CCTGCCAGTCAAGCTCGCTCTGTCCGTGCCCGCCACACCGACATGCCCAAGACCAG 255
287 CCTACAAAAGCAGCGCTCTATCGTCGTCGCCAGCCACACTGACATGCCCAAGCTAG 346
256 AAGTATCAGCCGCCCTCTACCAACAAGAACAGAGTCTCA---GAGAAGAAAGAGT 312
347 AAGTCCCGCTCCCTATCGACAACAAGAAAGAGAGTCTCAAGAGAGAGAGT 406
313 AATTTTGAAGACACAGTGAAGAGTGAAGAGAGAGAGAGTCAAGAGTGA- GAAGA 371
407 AATTTTGAAGACACAGTGAAGAGTGAAGAGAGAGAGAGTCAAGAGTGA- GAAGA 466
372 CCTCTGAGAGTGAAG 431
467 GCCTCCAG 526
432 TGTAAACATTTGATTCGGGCA-----AAAAATAGTTTGTATCATTTTCAAGATGG 485
527 GCAAAATCATGAAACACACTACCAAAATTAACATTAATTAATTAATTAATTAAGATGG 586
486 CATTCGCC 493
587 GCATTGCC 594

RESULT 10
AA913900/c
LOCUS
DEFINITION
AA913900 527 bp. mRNA linear EST 24-SEP-1998
c135405.s2 Soares_NFL_T.GBC_S1 Homo sapiens cDNA clone
IMAGE:1525496.3 similar to gb:X57025.rna1 INSULIN-LIKE GROWTH
FACTOR 1A PRECURSOR (HUMAN)), mRNA sequence.
ACCESSION
AA913900
VERSION
AA913900.1 GI:3053292
KEYWORDS
EST.
SOURCE
human.
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 527)
NCI-CGAP <http://www.ncbi.nlm.nih.gov/ncicgap>.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index
Unpublished (1997)
JOURNAL
Contact: Robert Strausberg, Ph.D.
Email: cgapds-remail.nih.gov
This clone is available royalty-free through LMNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Insert Length: 870 Std Error: 0.00
Seq primer: -40ml3 fwd. ET from Amersham
High quality sequence stop: 97.
Location/Qualifiers
1..527
/organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_image="1525496"
/clone_lib="Soares_NFL_T.GBC_S1"
/lab_host="DH10B"
/note="Organ: pooled; Vector: pRT3D-Pac (Pharmacia) with
a modified polylinker. Site: 1; Not I; Site: 2; Eco RI.
Equal amounts of plasmid DNA from three normalized
libraries (fetal lung Nhl19w, testis NRT, and B-cell
NCI-CGAP_GCB1) were mixed, and ss circles were made in
vitro. Following HAP purification, this DNA was used as
tracer in a subtractive hybridization reaction. The driver
was PCR-amplified cDNAs from pools of 5,000 clones made
from the same 3 libraries. The pools consisted of
I.M.A.G.E. clones 297480-302087, 682632-687239,
726408-728711, and 729096-731399. Subtraction by Bento
Soares and M. Fatima Bonaldo."
BASE COUNT 125 a 134 c 119 g 149 t
ORIGIN
Query Match 58.0%; Score 299.8; DB 9; Length 527;
Best Local Similarity 85.5%; Pred. No. 3.9e-78; Mismatches 17; Indels 53; Gaps 5;
Matches 413; Conservative 0;

39 TCTTCAAGTCTGTGTGAGACAGGGGCTTTATTTTCACAGGCCACAGGATAGGCTC 98
527 TCTTCAAGTCTGTGTGAGACAGGGGCTTTATTTTCACAGGCCACAGGATAGGCTC 468
99 CAGAGTCGAGAGGGGCGCTCAGACAGCATCGTGAATGCTCGCTCCGAGAGCTGTA 158
467 CAGAGTCGAGAGGGGCGCTCAGACAGCATCGTGAATGCTCGCTCCGAGAGCTGTA 408
159 TCTAAGAGAGGCTGAGATGTATTGCGACCCCTCAAGCCCTGCGCAAGTCAAGTGGCTGT 218
407 TCTAAGAGAGGCTGAGATGTATTGCGACCCCTCAAGCCCTGCGCAAGTCAAGTGGCTGT 348
219 CCGTGGCCAGGCGCCACACAGCATGCCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 278
347 CCGTGGCCAGGCGCCACACAGCATGCCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAG 311
279 CAGAGACGAGAGTCTCAGAGAAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 338
310 -----AAGGAGAGTCTTTGAAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 277

OY 339 GTGAGGAAACAGAACTACAGATGTA-GAAGACCTTCTGAGGATGAAGAGACAG 397
 DB 276 GTGAGGAAACAGAACTACAGATGTAAGAGACCTTCTGAGGATGAAGAGATGACAT 217
 OY 398 GCCACCCGAGACCTTGTCTGACAC-AGTTACTGCT-ATAACATTGGAATCCGCCAA 455
 DB 216 GCCACCCGAGATCCTTGTCTGACAGACTTACCTGTTAACTTTGGAACACTACCA 157
 OY 456 AAATAAGTTGATCATTTCACAAAT-GGCATTTCCTCCCAATGAATACACACTAA 514
 DB 156 AAATAAGTTGATCATTTCACAAATGAGGCGCTTCCCAATGAATACACACTAA 97
 OY 515 CAT 517
 DB 96 CAT 94

RESULT 11
 A1876493/c
 LOCUS
 DEFINITION A1876493 642 bp mRNA linear EST 21-JUL-1999
 U359b10.x1 Sugano mouse liver mlia Mus musculus cDNA clone
 IMAGE:1924219 3 similar to gb:X57025.fna1 INSULIN-LIKE GROWTH
 FACTOR IA PRECURSOR (HUMAN); gb:X04482 mouse mRNA for
 preproinsulin-like growth factor IB (MOUSE); mRNA sequence.
 A1876493
 A1876493.1 GI:5550542
 EST.

ACCESSION
 VERSION
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS

TITLE
 JOURNAL
 COMMENT

house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 642)
 Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T.,
 Underwood, K., Stepec, M., Theising, B., Allen, M., Bowers, Y., Person,
 B., Swaller, T., Gibbons, M., Page, D., Harvey, N., Schurk, R., Ritter,
 E., Kohn, S., Shin, T., Jackson, I., Cardenas, M., McCann, R.,
 Waterston, R., and Wilson, R.
 The WashU-NCI Mouse EST Project 1999
 Unpublished (1999)
 Contact: Marra M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LIND; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:990511
 Seq primer: custom primer used
 High quality sequence stop: 257.
 Location/Qualifiers
 1. 642
 /organism="Mus musculus"
 /strain="C57BL"
 /db_xref="taxon:10090"
 /clone="IMAGE:1924219"
 /clone_1lb="Sugano mouse liver mlia"
 /sex="Female"
 /dev_stage="adult"
 /lab_host="DH10B"
 /note="Organ: liver; Vector: pME18S-FL3; Site: 1: DraIII
 (CACTGATG); Site: 2: DraIII (CAGCATGTG); 1st strand cDNA
 was primed with an oligo(dT) primer
 [ATGTGGCTTTTCTTTTCTTTT]; double-stranded cDNA was
 ligated to a DraIII adaptor [TGTGGCTTCTGAG], digested
 and cloned into distinct DraIII sites of the pME18S-FL3
 vector (5' site CACTGATG, 3' site CAGCATGTG). XhoI should
 be used to isolate the cDNA insert. Size selection was
 performed to exclude fragments <1.5kb. Library
 constructed by Dr. Sumio Sugano (University of Tokyo
 Institute of Medical Science). Custom primers for
 sequencing: 5' end primer CTCTGCTCTTAAAGCTGCG and 3' end
 primer CGACCTGCAAGCTGACGACA."

BASE COUNT 127 a 154 c 175 g 185 t 1 others
 ORIGIN
 Query Match 56.0%; Score 289.6; DB 9; Length 642;
 Best Local Similarity 78.9%; Pred. No. 4.5e-75;
 Matches 397; Conservative 0; Mismatches 99; Indels 11; Gaps 4;

OY 2 GACCGGAGCGCTCGGGGCTGAGCTGTGATGCTCTTCACTGCTGTGAGACA 61
 DB 503 GACCGAGAGACCTTTGCGGGCTGAGCTGTGATGCTCTTCACTGCTGTGAGACA 444
 OY 62 GGGCTTTTATTTCAACAAGCCACAGGGTATNGGCTCCAGAGTGGAGGGCGCTGAGA 121
 DB 443 GGGCTTTTCTTTCACAAAGGCCACAGGCTATGCTCCAGCATTTTGAAGGCACCTCAGA 384
 OY 122 CAGCATCGATGATGATGCTGCTTCCG-AGCTGTATCTAAGAGAGCTGAGATGTAT 180
 DB 383 CAGTCATATGTGATGATGTTGCTTCCGAGAGCTGTATCTGAGAGAGCTGNAGATGTAC 324
 OY 181 TCGGACACCCCTACACCTTGCACAGTCACTGCTGTCTGCTGCCACGACACACGAC 240
 DB 323 TGTGCCCACTGAACCTTCAAAAGACACCCGCTCTATCGTGCACGACACTGAC 264
 OY 241 ATGCCCAAGACCCAGAACTATCAGCCCATCTACCAACAAGACACGAACTCTCA--G 297
 DB 263 ATGCCCAAGACTCAAGACTCCCGCTCTATCGAACAAACAGAAACGAACTGGAAGG 204
 OY 298 AGAAGAAAGAAAGTACATTGTGAGAGACAGTGAAGAGAGTGCAGAAACAGAACTA 357
 DB 203 AGAAGAAAGAAAGTACATTGTGAGAGACAGTGAAGAGAGTGCAGAAACAGAACTA 144
 OY 358 CAGCATGTA-GAAGACCTTCTGAGAGTGAAGAGACAGGACACCCAGACCTTTG 416
 DB 143 CAGATGTAGAGAGAGCTCCACGAGACAGAAATGCCAATCATCAGCAGATCTTGG 84
 OY 417 CTCTGCAAGTACTCTGTAACATTGAAATCCGCCA-----AAAATAGTTGATC 470
 DB 83 CTGCTTGAGCAACCTCGCAAAACATCGAAACACTACCAATTAATAGTCAATA 24
 OY 471 ACATTCAAGATGATCTTCCC 493
 DB 23 ACATTCAAGATGATCTTCCC 1

RESULT 12
 AM495481/c
 LOCUS
 DEFINITION AM495481 499 bp mRNA linear EST 24-FEB-2000
 UI-M-BH3-auy-g-11-0-UI-s1 NIH.BMDP.M.S4 Mus musculus cDNA clone
 UI-M-BH3-auy-g-11-0-UI 3', mRNA sequence.
 ACCESSION AM495481
 VERSION AM495481.1 GI:7065762
 KEYWORDS
 SOURCE
 ORGANISM
 REFERENCE
 AUTHORS
 TITLE
 JOURNAL
 MEDLINE
 COMMENT

house mouse.
 Mus musculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 1 (bases 1 to 499)
 Bonaldo, M.F., Lennon, G. and Soares, M.B.
 Normalization and subtraction: two approaches to facilitate gene
 discovery
 Genome Res. 6 (9), 791-806 (1996)
 Contact: Chih, H
 National Institute of Mental Health
 6001 Executive Blvd. Room 7N-7190, MSC 9643, Bethesda, MD
 20892-9643, USA
 Tel: 301 443 1706
 Fax: 301 443 9890
 Email: mestrail.nih.gov
 The sequence contained an oligo-dT track that was present in the
 oligonucleotide that was used to prime the synthesis of first A
 strand cDNA and therefore this may represent a bonafide poly A
 tail. The sequence tag present in the cDNA between the NotI site

QY 300 AAGGAAGAGTACATTTGAGAACACAGTACAGGCGATGCGAGAAACAGACTACA 359
 |||||
 Db 228 AAGGAAGAGTACATTTGAGAACACAGTACAGGCGATGCGAGAAACAGACTACA 169
 QY 360 GGAATGA-GAAGACCTTCTGAGAGTGAAGAGGAGCCGCGAGAGACCTTCTCT 418
 |||||
 Db 168 GAATGAGAGAGGAGCTCCCGAGAGAACAGAAATGCGAGTACCGCAAGATCTTGT 109
 QY 419 CTGACAGTACTCTGTAACATTTGGATACCGGCA-----AAAATAGTTTATCAC 472
 |||||
 Db 108 GCTTGAGCAACCTGCAAAACATCGAGACACCGCCAAATATCAAAATGAGTTCAATAC 49
 QY 473 ATTCAAGAT-GGCAATTTCCCGCAATGAAATACAGTAAACAT 517
 |||||
 Db 48 ATTTCAGAGTGGCGATTTCCCTCATGAAATACAGTAAACAT 3

RESULT 14
 A1604642 882 bp mRNA linear EST 21-APR-1999
 LOCUS vm33808.y1 Strata gene mouse diaphragm (#937303) Mus musculus cDNA
 DEFINITION Clone IMAGE:1001007 5' similar to gb:M1568 INSULIN-LIKE GROWTH
 FACTOR IB PRECURSOR (HUMAN); gb:X04482 mouse mRNA for
 preproinsulin-like growth factor IB (MOUSE); mRNA sequence.

ACCESSION A1604642 GI:4613809
 VERSION A1604642
 KEYWORDS EST.
 SOURCE house mouse.
 ORGANISM Mus musculus.

REFERENCE 1 (bases 1 to 882)
 AUTHORS Maria M., Hillier L., Kucaba T., Martin J., Beck C., Wylie T., Underwood K., Steptoe M., Theising B., Allen M., Bowers Y., Person B., Swaller T., Gibbons M., Page D., Harvey N., Schurk R., Ritter E., Kohn S., Shih T., Jackson Y., Cardenas M., McCann R., Waterston R. and Wilson R.
 TITLE The WashU-NCI Mouse EST Project 1999
 JOURNAL Unpublished (1999)
 COMMENT Contact: Maria M/WashU-NCI Mouse EST Project 1999
 Washington University School of Medicine
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
 Tel: 314 286 1800
 Fax: 314 286 1810
 Email: mouseest@wustl.edu
 This clone is available royalty-free through LNL; contact the
 IMAGE Consortium (info@image.llnl.gov) for further information.
 MGI:565223

FEATURES
 source
 1. 882
 /organism="Mus musculus"
 /db_xref="taxon:10090"
 /clone="IMAGE:1001007"
 /clone_lib="Strata gene mouse diaphragm (#937303)"
 /tissue_type="diaphragm"
 /dev_stage="adult"
 /lab_host="SOLR (kanamycin resistant)"
 /note="Organ: diaphragm; Vector: pBluescript SK-; Site: 1;
 EcoRI; Site: 2; XhoI; Cloned unidirectionally from mRNA
 prepared from diaphragm muscle. Primer: Oligo dT. Average
 insert size: 1.5 kb. Uni-ZAP XR Vector: -5' adaptor
 sequence: 5' GAATTCGCGACGAG 3' -3' adaptor sequence: 5'
 CTCGAGTCTTTTCTTTTCTTTT 3'"

BASE COUNT 236 a 226 c 183 g 223 t 14 others
 ORIGIN
 Query Match 53.1%; Score 274.4; DB 9; Length 882;
 Best Local Similarity 75.6%; Fred. NO. 1.6e-70;

Matches 384; Conservative 0; Mismatches 115; Indels 9; Gaps 4;
 QY 1 GGACCGAGAGCGCTCTCGGGGCTGAGCTGGTGATCTCTTACGTTCTGTGGAGAC 60
 |||||
 Db 377 GGACAGAGAGACCTTTCGGGCTGAGCTGGTGATCTCTTACGTTCTGTGGAGAC 436
 QY 61 AGGGGCTTTTTCACCAAGCCACAGGGGATGCTCCAGAGTCGAGGGGCGCTCAG 120
 |||||
 Db 437 AGGGGCTTTTTCACCAAGCCACAGGGGATGCTCCAGAGTCGAGGGGCGCTCAG 496
 QY 121 ACAGCATCTGATGATGATGCTGCTCCGAGCTGTATCTAAGAGGCTGAGATGTAT 180
 |||||
 Db 497 ACAGCATCTGATGATGATGCTGCTCCGAGCTGTATCTAAGAGGCTGAGATGTAT 556
 QY 181 TGCCGACCCCTCAGGCTGCCAATGCTAGCTGCTCTCGTCCGAGGCGCCACACGAC 240
 |||||
 Db 557 TGCCGACCCCTCAGGCTGCCAATGCTAGCTGCTCTCGTCCGAGGCGCCACACGAC 616
 QY 241 ATGCCCAAGACCCGAGATATCAGCCCATCTACCAACAAGACAGAGTCTCAGAG- 299
 |||||
 Db 617 ATGCNNAGACTCAGAGATCCCGCTCTATCGACNNAGAGAAAGAGCTTGCAAG 676
 QY 300 --AAGGAAGAGTACATTTGAGAACACAGTACAGGAGTCCAGAAACAGACTA 357
 |||||
 Db 677 GAGAGGGAAGGAGTACTTTGAGGAACACAGTNGAGGAGTGCANGAAGACAGACTA 736
 QY 358 CAGATGTAGAGAGACCTTCTGAGAGTGAAGAGGAGGAGCCAGACCCCTTGC 417
 |||||
 Db 737 CCAGATGTAGAGAGAGCT-TCAGCGAGGAGAAATGCATCCCGNNAGATCTTGC 795
 QY 418 TCTGCACAGTACTCTGTAACATTTGGAATACCGGCCAA-----AAAATAGTTGATACA 473
 |||||
 Db 796 T-GCTTGAGTCACTGCAACATGCAACATGCAACATTTACCAATTACATTAAGTTCAATAC 854
 QY 474 TTTCAGATGCACTTCCCGCAATGAA 501
 |||||
 Db 855 ATACAAATGTCATTTCCCATTTGAA 882

RESULT 15
 A1478804/C 430 bp mRNA linear EST 14-APR-1999
 LOCUS tm52604.x1 NCI CGAP Kid1 Homo sapiens cDNA clone IMAGE:2161758 3'
 DEFINITION similar to gb:X57025_rnal INSULIN-LIKE GROWTH FACTOR IA PRECURSOR
 (HUMAN); mRNA sequence.
 ACCESSION A1478804 GI:4373617
 VERSION A1478804
 KEYWORDS EST.
 SOURCE human.
 ORGANISM Homo sapiens.

REFERENCE 1 (bases 1 to 430)
 AUTHORS NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
 TITLE National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
 Tumor Gene Index
 JOURNAL Unpublished (1997)
 COMMENT Contact: Robert Strausberg, Ph.D.
 Email: cgsb@remail.nih.gov
 Tissue Procurement: Christopher Moskalko, M.D., Ph.D., Michael R.
 Emmert-Buck, M.D., Ph.D.

CNA Library Preparation: M. Bento Soares, Ph.D.
 DNA Sequencing by: Washington University Genome Sequencing Center.
 Clone distribution: NCI-CGAP clone distribution information can be
 found through the T.M.A.G.E. Consortium/LNL at:
 www.bio.llnl.gov/dbtp/image/image.html
 Insert Length: 849 Std Error: 0.00
 Seq primer: -400P from Gibco
 High quality sequence stop: 411.
 Location/Qualifiers
 1. 430
 /organism="Homo sapiens"

FEATURES
 source

`/db_xref="taxon:9606"`
`/clone="IMAGE:2161758"`
`/clone_lib="NCI_GCAP_Kid11"`
`/lab_host="DH0B"`
`/note="Organ: kidney; Vector: p1773D-Pac (Pharmacia) with a modified polylinker: Site.1: Not I; Site.2: Eco R; plasmid DNA from the normalized library NCI_GCAP_Kid3 was prepared, and ss circles were made in vitro. Following HAA hybridization, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNA from a pool of 5,000 clones made from the same library (clonoids 1323376-1323911, 1456007-1456775, and 1500552-1502855). Subtraction by Bento Soares and M.`

```
/clone="IMAGE:2161758"
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/clone_lib="NCI_CGAP_Kid11"
```

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/lab_host="DH10B"
```

/note=Organ kidney; Vector: pTR30-*pac* (Pharmacia) with a modified polylinker: Site1: Not I; Site2: Eco RI; Plasmid DNA from the normalized library NCI CGAP Kid3 was prepared, and ss circles were made *in vitro*. Following HAV19c hybridization, this DNA was used as tracer in a subtractive hybridization reaction. The driver was PCR-amplified cDNA from a pool of 5,000 clones made from the same library (clone IDs 13223376-1323911, 1456007-1456775, and 15003532-1502835). Subtracted by Bento Soares and M.

BASE COUNT	96 a	93 c	103 g	138 t
ORIGIN				

ORIGIN

Query Match	51.98;	Score 268.2;	DB 9;	Length 430;
Best Local Similarity	95.08;	Pred. No. 9,2e-69;		

Best Local Similarity 95.0%; Pred. No. 9.2e-69;

Matches 320; Conservative 0; Mismatches 13; Indels 4; Gaps 4;

Oy	185	CACCCCTCAAGCCTGCGCAAGTCAGCGCGGTCTGTGTCGCGCCAGGCGCACACCGCACTGC	244
Db	430	CACCCCTCAAGCCTGCCAAGTCAGCTCGCTCTGTCTCGTCCAGCGCCACACCGCACTGC	371
Oy	245	CCAAAGACCAGAAGTATCAGCCCCCATCTTACCAACAGAACAAGAGTCTCAGAGAAGA	304
Db	370	CCAAAGACCAGAAGTATCAGCCCCCATCTTACCAACAGAACAAGAGTCTCAGAGAAGA	311
Oy	305	AAGSAGTACATTTGAAAGACACAAGTAGAGGAGTGTGAGCAACAACTAAGAGATG	364
Db	310	AAGSAGTACATTTGAAAGACCCAGTAGAGGAGTGCAGGAAACAAAGACTACAGATG	251
Oy	365	TA-GAAGACCCCTTCTGAGSAGTGAAGAAAGACAGGCCACGCGAGACCCCTTGTCTTGCA	423
Db	250	TAGGAAAGACCCCTCTGAGSAGTGAAGAGTGAATCCACCGAGATCCTTTGCTTGCA	191
Oy	424	C-AGTTACCTG-TAAACATTGGAAATACCGGCCCAAAAATAAGTTGATGACATTTCAAG	481
Db	190	CGAGTTACCTGTTAAACTTTGGAAACCCATCCAAAAAATAAGTTGATAAACTTTAAAG	131
Oy	482	AT-GGCTATTTCCCCCAATGAATATACCAAGTAAACAT	517
Db	130	ATGGGCGTTTCCCCCAATGAATATACCAAGTAAACAT	94

Db 430 CACCCCTCAGCCTGCCAAGTACGCTCGCTCTGTCCGTGCCACGCGCCACACCGACATGC 371

245 CCAGAGCCAGAAGTATCAGCCCCCATCTACCAACAAGAACCGAAGTCTCAGAGAAGGA 304

Db 3/0 CCAGACCCAGAGTATCAGCCCCCATCTACCAACAAGAACAAGTCTCAGAGAAGA 311

[illegible]

434 C-ACTTACCTG-TAAACATTGGAATACCCCGCAAAATAAATACCTTCATCAACAATTCAGAAAC 481

Db 190 CGAGTTACCTGTTAACTTTGGAACACCTACCAAAAATAAGTTGATACATTTAAAG 131

QY 482 AT-GGCATTTCGCCCAATGAATACACAGAAGTAAACAT 517

Db 130 ATGGGCGTTTCCCCCAATGAATACACAAGTAAACAT 94

Search completed: June 15 2003 18:18:21

Search completed: June 15, 2003, 18:18:21
Job time : 1104.81 secs

Job time : 1104.81 secs